

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:13 ; Search time 95.6613 Seconds
(without alignments)
1091.732 Million cell updates/sec

Title: US-10-056-052A-4

Perfect score: 1732
Sequence: 1 MVAADAPPAAGTDTITQNTLV.....NGSSGSDGDKVPEQDE 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1727	99.7	933	2	Q53653
2	1662	96.0	946	16	Q8NXJ1
3	1517	87.6	935	16	Q932C5
4	1517	87.6	989	16	Q99VJ4
5	1112	64.2	881	2	Q93MH7
6	416.5	24.0	961	16	Q99RD3
7	409	23.6	940	2	Q53652
8	393	22.7	943	16	Q8NU08
9	353	20.4	931	2	Q9K113
10	349	20.2	1056	16	Q8C072
11	349	18.9	1092	2	Q70022
12	326.5	18.7	1141	16	Q8NXS5
13	326.5	18.7	1038	16	Q99RD2
14	323.5	18.6	1166	2	Q8K489
15	323	18.6	566	2	Q8KR22
16	322.5	18.6	1015	16	Q8NU07

17	320.5	18.5	1141	16	Q99W46	Q99W46 staphylococ
18	320.5	18.5	1141	16	Q932F7	Q932F7 staphylococ
19	312.5	18.0	877	16	Q99R07	Q99R07 staphylococ
20	312.5	18.0	913	2	Q86476	Q86476 staphylococ
21	298	17.2	1171	2	Q9KMX6	Q9KMX6 staphylococ
22	291.5	16.8	907	16	Q8NUL0	Q8NUL0 staphylococ
23	257.5	14.9	1315	2	Q86488	Q86488 staphylococ
24	256.5	14.8	1347	16	Q8NXX6	Q8NXX6 staphylococ
25	240.5	13.9	1385	16	Q99W47	Q99W47 staphylococ
26	232	13.4	970	16	Q8D1L7	Q8D1L7 streptococ
27	232	13.4	1310	16	Q8E473	Q8E473 streptococ
28	230.5	13.3	955	16	Q8NXX7	Q8NXX7 staphylococ
29	229.5	13.3	953	16	Q99W48	Q99W48 staphylococ
30	210.5	12.2	947	2	Q86487	Q86487 staphylococ
31	204	11.8	1161	2	Q8R1J0	Q8R1J0 streptococ
32	204	11.8	1161	2	Q9X3M7	Q9X3M7 streptococ
33	201.5	11.6	1633	16	Q8CMP4	Q8CMP4 staphylococ
34	201.5	11.6	1733	2	Q9K1L4	Q9K1L4 staphylococ
35	197	11.4	1893	2	Q8KXW1	Q8KXW1 staphylococ
36	182	10.5	1039	2	F72534	P72534 streptococ
37	182	10.5	1160	2	Q8RM86	Q8RM86 streptococ
38	167.5	9.3	463	16	Q92DD5	Q92DD5 listeria in
39	157.5	9.1	462	16	Q8Y817	Q8Y817 listeria in
40	152	8.8	642	16	Q8E810	Q8E810 clostridium
41	151.5	8.7	3240	16	Q87P85	Q87P85 vibrio para
42	147.5	8.5	586	16	Q92F43	Q92F43 listeria in
43	142	8.2	766	2	Q9EXR6	Q9EXR6 bacillus sp
44	141	8.1	1386	16	Q92DL0	Q92DL0 listeria in
45	141	8.1	1681	5	Q81548	Q81548 plasmidium

ALIGNMENTS

RESULT 1

ID Q53653 PRELIMINARY: PRT: 933 AA.

AC Q53653/

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Clumping factor.

OC Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Newman;

RX MEDLINE=9424142; PubMed=8170386;

RT "Molecular characterization of the clumping factor (fibrogen receptor of Staphylococcus aureus.";

RT Mol. Microbiol. 11:237-248(1994).

CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY AN AMIDE BOND (BY SIMILARITY).

CC EMBL: Z18852; CAA79304.1; -.

DR PIR: S41539; S41539.

DR FDB: I067; 04-MAR-03.

DR GO: GO:0005618; C:cell wall; IEA.

DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0005215; F:transporter activity; IEA.

DR GO: GO:0006810; F:transport; IEA.

DR InterPro: IPR000515; BFD transp.

DR InterPro: IPR005877; Gpos_Y5IRK.

DR InterPro: IPR001899; Gram_pos_anchor.

DR Pfam: PF00746; Gram_pos_anchor; 1.

DR Pfam: PF04650; Y5IRK_signal; 1.

DR TIGRfam: TIGR01167; LpxTG_anchor; 1.

DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; 1.

DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.

KW Cell wall; Peptidoglycan-anchor.

SQ SEQUENCE 933 AA, 97058 MW, EBS1ADE2PFF759F4 CRC64;

Query Match 99.7%; Score 1727; DB 2; Length 933;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGDTINQTLNVTGIDSGTIVYPHOGAYKLVNGFSVPSAVKAGDTFKITVP 61
DB 221 VAADAPAGDTINQTLNVTGIDSGTIVYPHOGAYKLVNGFSVPSAVKAGDTFKITVP 280

QY 62 KELNLNGVSTAKVPPIMAGDQVLANGVIDSDGNVIYFTDYNTKDVAKATLMPAYID 121
DB 281 KELNLNGVSTAKVPPIMAGDQVLANGVIDSDGNVIYFTDYNTKDVAKATLMPAYID 340

QY 122 PENYKKTGNVTLGIGSTTANKTVLVDEYKKGFEVLSIKGTIDQDKNNNTYRQTIYV 181
DB 341 PENYKKTGNVTLGIGSTTANKTVLVDEYKKGFEVLSIKGTIDQDKNNNTYRQTIYV 400

QY 182 NPSGDNVIAPVLTLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVTN 241
DB 401 NPSGDNVIAPVLTLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVTN 460

QY 242 SVNITFEPNPKYKFEFNTPDQITTPYIVVNGHIDNSKGLALRSTLYGNSNIIMRS 301
DB 461 SVNITFEPNPKYKFEFNTPDQITTPYIVVNGHIDNSKGLALRSTLYGNSNIIMRS 520

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQDE 331
DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQDE 550

RESULT 2
Q8NXCJ1 PRELIMINARY; PRT; 946 AA.
AC Q8NXCJ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibrinogen-binding protein.
GN CLFA OR M0764.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 358:1819-1827(2002).
DR EMBL; AP004824; BAB94629.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR005877; Gpos_Y5IRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor.
DR Pfam; PF04650; Y5IRK_signal; 1.
DR TIGRFAMs; TIGR01167; lpxTG_anchor; 1.
DR TIGRFAMs; TIGR01167; lpxTG_anchor; 1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE 946 AA; 98238 MW; EFB838793201173 CRC64;

Query Match 96.0%; Score 1662; DB 16; Length 946;
Best Local Similarity 95.8%; Pred. No. 2.1e-84;
Matches 316; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 VAADAPAGDTINQTLNVTGIDSGTIVYPHOGAYKLVNGFSVPSAVKAGDTFKITVP 61
DB 220 VAADAPAGDTINQTLNVTGIDSGTIVYPHOGAYKLVNGFSVPSAVKAGDTFKITVP 279

QY 62 KELNLNGVSTAKVPPIMAGDQVLANGVIDSDGNVIYFTDYNTKDVAKATLMPAYID 121
DB 280 KELNLNGVSTAKVPPIMAGDQVLANGVIDSDGNVIYFTDYNTKDVAKATLMPAYID 339

QY 122 PENYKKTGNVTLGIGSTTANKTVLVDEYKKGFEVLSIKGTIDQDKNNNTYRQTIYV 181
DB 340 PENYKKTGNVTLGIGSTTANKTVLVDEYKKGFEVLSIKGTIDQDKNNNTYRQTIYV 399

QY 182 NPSGDNVIAPVLTLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVTN 241
DB 400 NPSGDNVIAPVLTLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVTN 459

QY 242 SVNITFEPNPKYKFEFNTPDQITTPYIVVNGHIDNSKGLALRSTLYGNSNIIMRS 301
DB 460 SVNITFEPNPKYKFEFNTPDQITTPYIVVNGHIDNSKGLALRSTLYGNSNIIMRS 519

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQDE 331
DB 520 MSWDNEVAFNNGSGSGDIDKPVVPEQDE 549

RESULT 3
Q932C5 PRELIMINARY; PRT; 935 AA.
AC Q932C5;
ID Q932C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibrinogen-binding protein.
GN FNB OR SAV0811.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
RA Kanemitsu M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003360; BAB56973.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR005877; Gpos_Y5IRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Y5IRK_signal; 1.
DR TIGRFAMs; TIGR01167; lpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Y5IRK_signal; 1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE 935 AA; 96950 MW; DC5A2D92CE3BA91C CRC64;

Query Match 87.6%; Score 1517; DB 16; Length 935;
Best Local Similarity 87.3%; Pred. No. 2.4e-76;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 VAADAPAGDTINQTLNVTGIDSGTIVYPHOGAYKLVNGFSVPSAVKAGDTFKITVP 61
DB 221 VAADAPAGDTINQTLNVTGIDSGTIVYPHOGAYKLVNGFSVPSAVKAGDTFKITVP 280

QY 62 KELNLNGVSTAKVPPIMAGDQVLANGVIDSDGNVIYFTDYNTKDVAKATLMPAYID 121
DB 281 KELNLNGVSTAKVPPIMAGDQVLANGVIDSDGNVIYFTDYNTKDVAKATLMPAYID 340

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QY 122 PENVKTGNVTLATGIGTNTANKTVLDYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 NPSGDNVIAPIVLTGNLKPNKPTDSNALIDQONTSIKYKVVADNADLSESYVNPENFEDVTN 400
QY 182 NPSGDNVIAPIVLTGNLKPNKPTDSNALIDQONTSIKYKVVADNADLSESYVNPENFEDVTN 241
DB 401 NPSGDNVIAPIVLTGNLKPNKPTDSNALIDQONTSIKYKVVADNADLSESYVNPENFEDVTN 460
QY 242 SVNITFPNPNQYKVEFTPDQDITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 461 QVRISFPNANQYKVEFTPDQDITTPYIVVNGHIDPASTGLALRSTLYGNSNIIMRS 520
QY 302 MSMDNEVAFNNGSGSGDIDKPVPEQDPE 331
DB 521 MSMDNEVAFNNGSGSGDIDKPVPEQDPE 550

RESULT 4
Q99VJ4 PRELIMINARY; PRT; 989 AA.
ID 099VJ4;
AC 099VJ4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)
DE Ribrogen-binding protein A, clumping factor.
GN CUPA OR SA0742.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Ito T., Kanamori M.,
RA Matsunari H., Maruyama A., Murakami H., Hoshiyama A., Mizutani-Uji Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kohara S., Goto S., Yabuuchi J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancel 357:1225-1240(2001).
DR EMBL; AF003131; BAB41975.1; -.
DR PIR; D89852; D89852.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001897; Gpos_Ysirk.
DR Pfam; PF00746; Gram_pos_anchor.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TRIGRAMS; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE 989 AA; 102407 MW; DAGE807539623467 CRC64;
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DB 341 PENVKTGNVTLATGIGTNTANKTVLDYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPIVLTGNLKPNKPTDSNALIDQONTSIKYKVVADNADLSESYVNPENFEDVTN 241
DB 401 NPSGDNVIAPIVLTGNLKPNKPTDSNALIDQONTSIKYKVVADNADLSESYVNPENFEDVTN 460
QY 242 SVNITFPNPNQYKVEFTPDQDITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 461 QVRISFPNANQYKVEFTPDQDITTPYIVVNGHIDPASTGLALRSTLYGNSNIIMRS 520
QY 302 MSMDNEVAFNNGSGSGDIDKPVPEQDPE 331
DB 521 MSMDNEVAFNNGSGSGDIDKPVPEQDPE 550

RESULT 5
Q93MH7 PRELIMINARY; PRT; 881 AA.
ID 093MH7;
AC 093MH7;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)
DE Receptin Fbl precursor.
GN FBL.
OS Staphylococcus lugdunensis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=28035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2342;
RA Nilsson M., Ahlen J., Frykberg L., Guss B.;
RT "A fibrinogen-binding protein of Staphylococcus lugdunensis."
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL. PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; AF048823; AAK95649.1; -.
DR GO; GO:0005613; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001897; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TRIGRAMS; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1
FT CHAIN 40
FT FT 881
SQ SEQUENCE 881 AA; 94251 MW; D4296C4959CAFI9B CRC64;
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Query Match 87.6%; Score 1517; DB 16; Length 989;
Best Local Similarity 87.3%; Pred. No. 2.6e-76;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
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QY 11 TDITNQLNTVTGIGDGTYYPHQAGYVKLNYSVNSAVKGDFTKITYPKELNLTGVT 70
DB 214 SDISNKLSTVATIEADITTPHKAERYNLNFRQAPDDVQADSDISITITPOLNLTGVT 273
QY 71 STAKVPIPMAGDQVLANGVIDSDGNVYFTPDYNTADVKATLTMPAYIDPENVKXTGN 130
DB 274 ATAKAPNIMAGDQVLANGVIDSDGNVYFTPDYNTADVKATLTMPAYIDPENVKXTGN 333
QY 131 VTLATGISTTANKTVLDYKYGKFNLSIKGTIDQIDKTNNTYRQTIYVPSGDNVIA 190
DB 191 PVLGTGNLKPNKPTDSNALIDQONTSIKYKVVADNADLSESYVNPENFEDVTNPNP 250
QY 334 VNLSTSGITTAKTATVLDYKYGKFNLSIKGTIDQIDKTNNTYRQTIYVPSGDNVIA 393
DB 394 PVLGTGNLKPNKPTDSNALIDQONTSIKYKVVADNADLSESYVNPENFEDVTNPNP 453
QY 251 NQYKVEFTPDQDITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRSMDNEVAF 310
DB 454 GIVQINTEBDQINSYVIVVNGHIDPNSKGLALRSTLYGNSNIIMRSMDNEVAF 513
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QY 311 NNNGSGGDIKRPVPEQDPE 331
DB 514 HAAGSGGDIKRPVPEQDPE 534

RESULT 6
Q99RD3 PRELIMINARY; PRT; 961 AA.
ID Q99RD3
AC Q99RD3
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE FMB protein (Fibronectin-binding protein homolog).
GN FMB OR SAV2502 OR SA2290.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
[1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoya A.,
RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Masahita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003365; BAB58664.1; -
DR EMBL; AP003337; BAB43593.1; -
DR PIR; G90053; G90053.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Complete proteome.
SQ SEQUENCE 961 AA; 106010 MW; 364940F84EA4101 CRC64;

Query Match 24.0%; Score 416.5; DB 16; Length 961;
Best Local Similarity 29.1%; Pred. No. 3.8e-15;
Matches 101; Conservative 69; Mismatches 144; Indels 33; Gaps 9;

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DB 390 AKDDTSKFEVYTKNVLSTNSGTYLNLGDDLN--SKDYIKYGEYDQNAK-DLNR 446
QY 288 STLYGNSNIWR-----SMKWNEVAFNNNGSGGDIKRPV 326
DB 447 THLSGHKYYYPYYPYYPVOLTNNNGVAFYNNNAKDGDKRPND 493

RESULT 7
Q93682 PRELIMINARY; PRT; 940 AA.
ID Q93682
AC Q93682
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibronectin binding protein B.
GN FNB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RX MEDLINE=92111475; PubMed=1837266;
RA Johnson K., Sigas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene."
RL Eur. J. Biochem. 202:1041-1048(1991).
CC - SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; X62892; CAA44726.1; -
DR PIR; S19702; S19702.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fb_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind; 2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs; TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

Query Match 23.6%; Score 409; DB 2; Length 940;
Best Local Similarity 28.9%; Pred. No. 9.7e-15;
Matches 101; Conservative 72; Mismatches 131; Indels 46; Gaps 11;

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DB 436 NA-SUBFOTHLPGYNYTYTNSLTKNGVAFYSSNAGDGKDKLEPTI 484

RESULT 8

Q8NTU8 PRELIMINARY; PRT; 943 AA.

AC Q8NTU8 PRELIMINARY; PRT; 943 AA.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FnbB protein.
 GN FNB OR MM2420.
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiratake K.,
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."
 RL Lancet 359:1819-1827(2002).
 DR EMBL: AB004830; BAB96285.1;
 DR GO: GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR InterPro: IPR004237; Fm_bind.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fm_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Complete proteome.
 SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 22.7%; Score 393; DB 16; Length 943;
 Best Local Similarity 29.3%; Pred. No. 7.5e-14;
 Matches 103; Conservative 64; Mismatches 141; Indels 44; Gaps 11;

DB 2 VAADAPAGDTITNLTNTVVGIDSGT-----TVYPHQAGYKLVNAGFSVNSA 50
 155 VVEEAKATGDTVSK-----VEVEEGSEIYGHNNKETNVNPNHARVTLTKYKMKPEDGI 209
 QY 51 VKGDFTKITVYKRELNLNGVTSKAVPPIMA-GQVULANGVIDSGNVITFTPDYVNTKTD 109
 DB 210 KPDDYDFLTISNNVETHGHSPLRKVPDLSKDNILAVGVKDERKIRTFPDYINNNKN 269
 QY 110 VKRTLTMPAVIDPENYKGTGNVTLATIGSTTANKTFLVDY-----EKYGEFYNLSIKGT 164
 DB 270 LMAELMLNLFIDPTVTKGKQVVEVXLGHNKSKSFIDKLDGVADNNG---VTVNR 325
 QY 165 IDIDIKNTNTYRQTIYVNSGDNVIAVLTGNIKPTDSNALIDQNTSITKYKVDNAAD 224
 DB 326 ITLLDKENSKIRHIAINPKKSDMTSITINGPFA---KGLYTGVPVTKYVEYLRSDE 381
 QY 225 LSSSYFVN---PENFEDVTSVN--ITFPNQCXYEFNTPDDQITTPYIVVNGHIDN 279
 DB 382 LPSVYANTNDQKFDVNTDMSDKLTLSNNGSYKL---TLDLNKKSYVVSFEQKYNEN 438
 QY 280 SKQDLALRSTLYGNSNITWR-----SMGWDNEVAFNNGSGSDGIDKPVVP 326
 DB 439 DK-ELFRTIHLGYNHYGYYYYPVSLTWNGVAFYSNNAQDGDKXNDP 489

RESULT 9
 Q9KI13 PRELIMINARY; PRT; 931 AA.

AC Q9KI13:
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fibrinogen-binding protein Sdrg.
 GN SDRG.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K28;
 RX MEDLINE=20340957; PubMed=10878118;
 RA McCrea K.W., Hartford O., Davis S., Ni Eidhin D., Lina G.,
 RA Speziale P., Foster T.U., Hook M.;
 RA "The serine-aspartate repeat (Sdr) protein family in Staphylococcus
 RT epidermidis."
 RT Microbiology 146:1535-1546(2000).
 RL -1 SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
 CC AN AMIDE BOND (BY SIMILARITY).
 CC EMBL: AF245042; AAF72510.1;
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR008454; Cna_B.
 DR InterPro: IPR005877; Gpos_YsIRK.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF05738; Cna_B; 2.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; YsIRK_signal; 1.
 DR TIGRfams: TIGR01167; LpxTG_anchor; 1.
 DR TIGRfams: TIGR01168; YsIRK_signal; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Cell wall; Peptidoglycan-anchor.
 SQ SEQUENCE 931 AA; 102955 MW; 591E657D97027116 CRC64;

Query Match 20.4%; Score 353; DB 2; Length 931;
 Best Local Similarity 30.6%; Pred. No. 1.2e-11;
 Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

DB 13 ITNOLTNWTVGI-DSGTTVPHQAGYKLVNAGFSVNSA VKGDTFKITVYKRELNLNGVTS 71
 DB 285 VTDD--SITSGYDSDSGIKAHDAENLIYDVFEDVDKVSQDPTMVIDKNTVPSDLT 342
 QY 72 TAKVPPIMAGD-QVLANGVID-SDGNVITYFTPDYVNTKDVKATLTMPAIDPENYKGT 129
 DB 343 SPALPKIKDNGSELIATGTYDNTNRQITFTPDVVDYENIKAKLTKTYSIDSKVPPNN 402
 QY 130 --NVTLATIGSTTANKTFLVDYEKYGEFYNLSIKGTIDIDIKNTNTYRQTIYVNSGD 186
 DB 403 TKLDEVKXTALSS--VAKTITVEQKNEKNTALQSMFTNIDKNTVEQTIYINFL-- 458
 QY 187 NVIAPVLTGNIKPTDSNALIDQNTSITKYKVDNAADLSBSYFV-NPENFEDVTSVNT 245
 DB 459 RYSAKETVWNSGCGDESDTIDISTIKYKVDNNDLPSNRIVYSYEDVETNDVYA 518
 QY 246 TFPNPNQCXYEFNTPDDQITTPYIVVNGHIDPSKGD-----LALRSTLYGNSNII 298
 DB 519 QLGNNNDVNIIFG---NIDSPYIIKVISKIDEN-KDYTYTIOQTYVMQTTINYEGB-- 571
 QY 239 WRSMSWMDNEVAFNNGSGSDGIDKPVVPEQ 328
 DB 572 FRTASVDNTIAFSTSSGQGG-DLP--PEK 598

RESULT 10
 Q8CQ72 PRELIMINARY; PRT; 1056 AA.
 AC Q8CQ72:
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding
 DE protein.

GN SE0331.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB016745; A003928.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR008454; Cna_B_2.
DR InterPro: IPR008477; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF05738; Cna_B_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KM Complete Proteome.
SQ SEQUENCE 1056 AA; 115728 MW; 015869A9E5CA2723 CRC64;

Query Match 20.2%; Score 349; DB 16; Length 1056;
Best Local Similarity 30.3%; Pred. No. 2.4e-11;
Matches 100; Conservative 61; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNVTG-I-DSGTTYPHQAGYVKLNGFSVPNSAVKDTFKITVPEKELNLTGVS 71
DB 287 VTDQ--SITEGYDSDSGVIAKHAENLIYVTFEVDKVKSGDTMTVVIDKKTVPESDLTD 344
QY 72 TAKVPPIMAGD-QVLANGVIDS-DGNVITFTDYNTKDVAKTLMPAYIDPENVKKTG 129
DB 345 SFTIPKIKNSGEIITGTGYDNKQKITFTFDYVKENIRAHKLTSYIDSKVPENN 404
QY 130 ---NVLATIGSTTANKTVLVDEYKGFYNLSIKGITDIQIDKNTNTRQTIYVNP 186
DB 405 TKLDVEKTKALSS--VNKTIIVEYGRPNENRANLQSMFTNIDTKHTEQTIYINPL-- 460
QY 187 NVIAPVLTGKLNKNTSNALIDQNTSIRYKVDNAADSESYFV-NPENFEVDYNSVNI 245
DB 461 RYSAKETNVNISNGEGSTIIDSTIIKYKVGDNQLPDSNRITYSEYEDVINDDYA 520
QY 246 TFPENPQYKVEFTPDQITTPYIVVNGHIDPNSKGD-----LALSTLYGYSNII 298
DB 521 QLGNNNDVNIINFG---NIDSPYIIKVIKSKYDPN-KDVTYTIQVTVMTQTTINEYGE-- 573
QY 299 WRSMGNDNEVAFNNGSGSGDIDKPYVPEQ 328
DB 574 FRTASYDNTIAFSTSSGQGG-DLP--PEK 600

RESULT 11
ID 070022; PRELIMINARY; PRT; 1092 AA.

AC 070022; (TREMUREL. 07, Created)
DT 01-AUG-1998 (TREMUREL. 07, Last sequence update)
DT 01-OCT-2003 (TREMUREL. 25, Last annotation update)
DE Fibrinogen-binding protein precursor.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB;
RX MEDLINE=98261511; PubMed=9596732;
RA Nilsson M., Frykberg L., Flock J.I., Pei L., Lindberg M., Guss B.;
RT "A fibrinogen-binding protein of Staphylococcus epidermidis";
RL Infect Immun 66:2666-2673(1998).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).

DR EMBL: Y17116; CAAT6638.1; -
DR PIR: T30214; T30214.
DR GO: GO:0005619; C:cell wall; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR008454; Cna_B.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF05738; Cna_B_2.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
DR TIGRFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PSS0847; GRAM_POS_ANCHORING; 1.
KM Cell wall; peptidoglycan_anchor; signal.
FT SIGNAL 1 51
FT CHAIN 52 1092
SQ SEQUENCE 1092 AA; 119292 MW; 6542BC39AAB984 CRC64;

Query Match 20.2%; Score 349; DB 2; Length 1092;
Best Local Similarity 30.3%; Pred. No. 2.5e-11;
Matches 100; Conservative 61; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNVTG-I-DSGTTYPHQAGYVKLNGFSVPNSAVKDTFKITVPEKELNLTGVS 71
DB 287 VTDQ--SITEGYDSDSGVIAKHAENLIYVTFEVDKVKSGDTMTVVIDKKTVPESDLTD 344
QY 72 TAKVPPIMAGD-QVLANGVIDS-DGNVITFTDYNTKDVAKTLMPAYIDPENVKKTG 129
DB 345 SFTIPKIKNSGEIITGTGYDNKQKITFTFDYVKENIRAHKLTSYIDSKVPENN 404
QY 130 ---NVLATIGSTTANKTVLVDEYKGFYNLSIKGITDIQIDKNTNTRQTIYVNP 186
DB 405 TKLDVEKTKALSS--VNKTIIVEYGRPNENRANLQSMFTNIDTKHTEQTIYINPL-- 460
QY 187 NVIAPVLTGKLNKNTSNALIDQNTSIRYKVDNAADSESYFV-NPENFEVDYNSVNI 245
DB 461 RYSAKETNVNISNGEGSTIIDSTIIKYKVGDNQLPDSNRITYSEYEDVINDDYA 520
QY 246 TFPENPQYKVEFTPDQITTPYIVVNGHIDPNSKGD-----LALSTLYGYSNII 298
DB 521 QLGNNNDVNIINFG---NIDSPYIIKVIKSKYDPN-KDVTYTIQVTVMTQTTINEYGE-- 573
QY 299 WRSMGNDNEVAFNNGSGSGDIDKPYVPEQ 328
DB 574 FRTASYDNTIAFSTSSGQGG-DLP--PEK 600

RESULT 12

ID 08NXX5; PRELIMINARY; PRT; 1141 AA.

AC 08NXX5;
DT 01-OCT-2002 (TREMUREL. 22, Created)
DT 01-OCT-2002 (TREMUREL. 22, Last sequence update)
DT 01-OCT-2003 (TREMUREL. 25, Last annotation update)
DE Ser-Asp rich fibrinogen-binding bone sialoprotein-binding
protein.
OS SDRF OR M00518.
OC Staphylococcus aureus (strain M02).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA";
RL Lancet 359:1819-1827(2002).
RE EMBL: AF004823; BAB94383.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR008454; Cna_B.
DR InterPro: IPR005877; Gpos_YsIRK.

DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF05738; Cna_B; 3. anchor; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
 KW Complete proteome.
 SQ SEQUENCE 1141 AA; 123997 MW; 372586050A332C CRC64;

Query Match 18.9%; Score 326.5; DB 16; Length 1141;
 Best Local Similarity 31.5%; Pred. No. 4.7e-10;
 Matches 112; Conservative 52; Mismatches 137; Indels 55; Gaps 18;

DR 2 VAADPAAGTITNLTNTV-----VGIIDSGTIVYPHQAGVYKLVNYSVNSAVKGDITF 56
 DB VAQPAAVASNNV--NDLIVTKQITIVGDKDVAAMHGGKIDIEFTETITNKVKKGDITM 322
 QY 57 KI-----TVPKELNNGVTSTAKVPPIMAGD---QVLANGVID--SDGNVIYTFDYVNTK 107
 DB 323 TINYDKNVIIPSDL-----TDKNPDIDITPDSGEVIAGTFDKATKQITVTFDYDKY 375
 QY 108 DDVKAITIMPATIDPENV--KKTGNVTLATIGSTANKTVLVDEKKGKRYNLSIKGTI 165
 DB 376 EDIKRLLTLYSTIDKKVFNETSINLTFATAGKETSQN--VTVDYQDPVHGDNSIQIF 433
 QY 166 DQIDKTNNYRQTIYVNP---SGDNVIAPVL-----TGNLKPNVDSNALIDQONTSIKV 216
 DB 434 TKLDDKQITIEQIVYVPLKKSANTKTVDIAGSQVDYGNIKLNGS--TIID-QNTLKV 491
 QY 217 YKVDNAALDSSEYFV--NPENFEDVTSVNTTFPNPNQYKVEFNPD--DQITPIYIVYNG 274
 DB 492 YKVNDDQCPQSNRYIDPSQYEDVTSQ---FDNKKSPSNVVALTFDGINSAVIKIVS 547
 QY 275 HIDEPSKGLP-----ALRST-LYGVNSNIIRMSMWDNEVAFNNGSGSGGIGIXP 323
 DB 548 KTFPIISDELIDIAQGTSMRTDKYQ-----YNVAGYGNFIVTSNDSGGGIGYKRP 598

RESULT 13
 Q99RD2 PRELIMINARY; PRT; 1038 AA.
 AC Q99RD2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Fnb protein (Fibronectin-binding protein homolog).
 GN FNB OR SAV2503 OR SA2291.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxId=158878; 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES= S. aureus (strain Mu50), and S. aureus (strain N315);
 RX MEDLINE=2111952; PubMed=11418146;
 RA Kuroda M., Ohba T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-T., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanemori M., Matsumaru H., Maruyama A., Muzikami H., Hosoyama A.,
 RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi Y.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003365; BAB58665.1; -;
 DR EMBL; AP003137; BAB43594.1; -;
 DR PIR; H90053; H90053.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR004237; Fnb_bind.

DR InterPro: IPR005877; Gpos Ysirk.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF02986; Fnb_bind; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.
 DR TIGRFAMs: TIGR01167; LpxTG_anchor; 1.
 DR TIGRFAMs: TIGR01168; Ysirk_signal; 1.
 DR PROSITE: PS0847; GRAM_POS_ANCHORING; 1.
 KW Complete proteome.
 SQ SEQUENCE 1038 AA; 113618 MW; 666BF62BFBEB12 CRC64;

Query Match 18.7%; Score 324.5; DB 16; Length 1038;
 Best Local Similarity 26.9%; Pred. No. 5.4e-10;
 Matches 91; Conservative 68; Mismatches 154; Indels 25; Gaps 11;

DR 10 GTDITNLTNTVTVGDS--GTVYVPHQAGVYKLVNYSVNSAVKGDITFVPEKLN 67
 DB 189 GIDVTSKTVESGSIAPGKNVPEHAGQVYKLVKAFADQKRGDYFDFTLSNNVNY 248
 QY 68 GVTSTAKVPPIMAGDQVLANGVIDSDGNVYTFDYVNTKDYKATLTMPATIDPENYK 127
 DB 249 GVTSTAKVPEIKNGSVVMAATGEILGNGNIRYFTFNEIEHKVEVTANLEINLFIDKTVQS 308
 QY 128 TGNVTLATIGSTANKTVLVDEKKGKRYNLSIKGTIDQIDKTNNYRQTIYVNPSCGN 187
 DB 309 NGQKITTSKLNGBETETKITPVYVNGSVNSYTNVNGSITFPKESNKPTHIAVIRPAGN 368
 QY 188 VIAPV--LTGNLKPNVDSNALIDQONTSIKVK--VDNAALDSSEYFNPEN--FEDVTVS 242
 DB 369 QSNVTSVTVGL--TGSNLAGQQLP--KVVEYVLGKDELPSVYANTSDTKRFDVYKE 424
 QY 243 VN--TFPNPNQYKVEFNPPDQITPIYVYVNGHIDPSKDDLRLSTLYG-----YVS 295
 DB 425 MNKSLVQDNGSISLNL---DKLDKTVIHYTGEVLYGS--QVNFRELYGYPERAYKS 479
 QY 296 NIWRS--MSWDNEVAFNNGSGSGDIDKRPVPEQDF 331
 DB 480 YVYGGVRLTWNGDLVYLSNKADGNKNGKQIIGDNDFE 517

RESULT 14
 O86489 PRELIMINARY; PRT; 1166 AA.
 ID O86489;
 AC O86489;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Sdr E protein.
 GN SDR E.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Newman;
 RX MEDLINE=99098700; PubMed=9884231;
 RA Josefson E., McCrea K., Ni Eidhin D., O'Connell D., Cox J., Hook M.,
 RA Foster T.J.;
 RT "Three new members of the serine-aspartate repeat protein multigene
 family of Staphylococcus aureus";
 RL Microbiology 144:3387-3395(1998).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
 AN ANIDE BOND (BY SIMILARITY).
 DR EMBL; AJ005647; CA06552.1; -;
 DR PIR; T28680; T28680.
 DR GO; GO:0005618; C:cell wall; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008454; Cna_B.
 DR InterPro; IPR005877; Gpos_Ysirk.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam: PF05738; Cna_B; 3. anchor; 1.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR Pfam: PF04650; Ysirk_signal; 1.

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DR TIGRFAMS; TIGR01167; LEXTG anchor: 1.
DR TIGRFAMS; TIGR01168; YSIRK signal: 1.
DR PROSITE; PS50847; GRAM POS ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 1166 AA; 126548 MW; 750A7B0135287D4A CRC64;

Query Match 18.7%; Score 323.5; DB 2; Length 1166;
Best Local Similarity 31.2%; Pred. No. 7,1e-10;
Matches 111; Conservative 53; Mismatches 137; Indels 55; Gaps 18;

QY 2 VADAPAGTDITNLTNTV-----VGIDSGTIVYPRQAGYKLVNPGSVNSAVKGDTE 56
DB 269 VAQPAVAVNNV-NDLIKTKQTIKVGDEKQVAAAHQKDI EYDTEFTIDNKYKKGDTM 327
QY 57 KI-----TPKELNNGVTSTAKVPIMAGD---QYLANGVID-SDGNVIYTFDYNVTK 107
DB 328 TINYDKNVI PSDL-----TDKNDFIDITDPSGEVIAKGFDPKAKQIYTFIDYDKY 380
QY 108 DVYKATLTWPAYIDPENV--KKTGNVTLATGIGSTANKTVLDYEKYKGFYNLSIKGTI 165
DB 381 EDIKSLTLYSYIDKKTIVNFTSNLTFATAGKETSON--VTVDYQDPWVHGDNSIQSIF 438
QY 166 DQIDKTNNTYRQTIYVNP--SGDNVIAVL-----TGNLKPNTDSNALIDQNTSIKY 216
DB 439 TKLDEKQKTEIQIYVNPPLKKSATNKTVDIAGSQVDYDGNIKLGNGS--TIID-QNTEIKY 496
QY 217 YKVDNADLSSESYFV-NPENFEDVTNSVNTFPNPQYKVEFTPP-DQITTPYIVVNG 274
DB 497 YKVNSDQQLPQSKRIYDFSGYEDVTSQ---FDNKSFSNNVATIDFGDINSAYIIKIVS 552
QY 275 HNDPNSKGLD-----ALRST-LYGVNSNIIMRSMWNEVAFNNGSGSGGIDKP 323
DB 553 KYPTISDGEHDIAGTSMRTTDKGY-----YVAGYSNFIYTSNDTGSGDGTVPK 603

RESULT 15

Q8KR22 PRELIMINARY; PRT; 566 AA.
AC Q8KR22;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Serine-aspartate repeat protein (Fragment).
OS Staphylococcus caprae.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=29380;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=89320;
RA Aubert S., Allignet J., Dyke K.G.H., Ryden C., El Solh N.;
RT "Staphylococcus caprae gene encoding a serine-aspartate repeat
protein."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048594; AAL08114.1; -
FT NON TER 1
SQ SEQUENCE 566 AA; 62896 MW; 0506759E2AFD3284 CRC64;

Query Match 18.6%; Score 323; DB 2; Length 566;
Best Local Similarity 29.7%; Pred. No. 3.1e-10;
Matches 89; Conservative 58; Mismatches 121; Indels 32; Gaps 12;

QY 4 ADAPAGTDITNLTNTVVGIDSGTIVYPRQAGYKLVNPGSVNSAVKGDTEFTKIVPKR 63
DB 265 ANSQGQSSNNDKI-NDVSFNVSKSPDPNHSQSYDLNASFVNGKIKEGDYFTVKYQOR 323
QY 64 LNLNG-----VSTAKYPIIM-AGDOYLANGVIDSDGNI-VTFDYNVTKDVKATLT 115
DB 324 VTAVGDVNYEKLNQMKVRLTNANGDVVANGLYDVNSKTVKTFINFNDRNNIKGNRK 383
QY 116 MPAYIDPENYKKTGNVTLATGIGSTANKTVLDYER---YGFYNLSIKGTIDQID-- 169
DB 384 LPFTDKRKNPHSGNSYSTFNIAIDKNYETELNISYDSFYQGIKDAYGPNISSFTIDILH 443

QY 170 KTNNTYRQTIYVNP-----GDNVIAVLGNLKPNTDSNALIDQNTSIKYKYVDNAD 224
DB 444 SGSEDPKQKTYNMENTYNSNV---RIGYQTOGSKSSTIID-KNTEFKTYQKDAHQ 499
QY 225 LSESYF--VNPENFEDVTNSVN--ITFPNPQYKVEFTPDQITTPYIVVYNGHIDPNS 280
DB 500 LSESYNDTNSNLVDVTNNFNGMITYNSDNSVNIQFG---HIDQAYIIIEVGKYSKS 555

Search completed: March 26, 2004, 05:07:43
Job time : 101.661 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:51:26 / Search time 19.9539 Seconds
(without alignments)
863.752 Million cell updates/sec

Title: US-10-056-052a-4

Perfect score: 1732
Sequence: 1 MVADAPAGAGTDITNLTNV.....NGSGSGDIDKPVVEQPDF 331

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	331	19.1	1018	FNBA_STRAU
2	129	7.4	762	SLAP_ACEKI
3	128	7.4	2021	OMPA_RICCN
4	127	7.3	642	FLID_CAMUE
5	121.5	7.0	2249	OMPA_RICRI
6	120.5	7.0	612	DNAC_OCEIH
7	119.5	6.9	344	GLP10_DICDI
8	117	6.8	856	ALET_AZOVI
9	115.5	6.7	928	PML1_CHLPN
10	114.5	6.6	1643	OMPB_RICPR
11	114	6.6	738	YO13_BPL2
12	113.5	6.6	1238	SLAP_BACST
13	113.5	6.6	1250	YFAL_ECOLI
14	113.5	6.6	1902	PIP_LACAC
15	113.5	6.6	1902	P2P_LACPA
16	113.5	6.6	1286	ALDA_ECOLI
17	113	6.5	1394	HAP_HAELN
18	113	6.5	1394	P2P_LACIC
19	112	6.5	1902	YIOG_YEAST
20	111	6.4	1176	SLAP_BACSH
21	110.5	6.4	1645	OMPB_RICTY
22	110.5	6.4	1183	CNA_STRAU
23	110	6.4	760	SIX4_HUMAN
24	109.5	6.3	2003	CSG_HALVO
25	108.5	6.3	827	YVEE1_ECOLI
26	108	6.2	2358	Y795_MERTI
27	108	6.2	504	HAPI_HAELN
28	107.5	6.2	1409	OMPB_RICCN
29	107.5	6.2	1655	API_KTOLA
30	107	6.2	583	Q9V8R9_drosophila
31	107	6.2	1698	41 DROME
32	106.5	6.1	1181	ITAA2_HUMAN
33	106.5	6.1	1181	PI7301 homo sapien

34	106	6.1	1562	1	SPAP_STRMU	P23504 streptococc
35	105.5	6.1	402	1	FLGE_SALTY	P16822 salmonella
36	105.5	6.1	444	1	SLAP_LACAC	P35829 lactobacilli
37	105.5	6.1	544	1	PME3_LYCES	Q96576 lycopersico
38	105.5	6.1	2452	1	RPA1_PLAFO	P14248 plasmodium
39	105	6.1	537	1	TER6_STRPV	P16481 streptococc
40	105	6.1	655	1	YKDA_MYCCA	P45615 mycoplasma
41	105	6.1	906	1	Y010_CIOAB	Q97828 clostridium
42	105	6.1	928	1	PMP9_CHLPN	Q92398 chlamydia p
43	105	6.1	1565	1	PAC_STRMU	P1657 streptococc
44	104.5	6.0	448	1	FIBR_ADEP3	Q83457 porcine ade
45	104.5	6.0	870	1	P100_HSV6U	Q00701 human herpe

ALIGNMENTS

RESULT 1

FNBA_STRAU STANDARD; PRT; 1018 AA.

AC P14738; 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN FNBA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;

NP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signes C., Rautci G., Joensen K., Lindgren P.-E.,
"Nucleotide sequence of the gene for a fibronectin-binding protein
from Staphylococcus aureus: use of this peptide sequence in the
synthesis of biologically active peptides."

RT RT
RL Proc. Natl. Acad. Sci. U.S.A. 86:1699-703(1989).
CC -1- FUNCTION: THE ABILITY OF BACTERIA TO BIND FIBRONECTIN HAS BEEN
PROPOSED AS A VIRULENCE FACTOR ENABLING BACTERIA TO COLONIZE
WOUND TISSUES AND BLOOD CLOTS. BINDING OF PLASMA FIBRONECTIN TO
THE BACTERIAL SURFACE MIGHT BLOCK ADHESION RECEPTORS ON S. AUREUS,
THUS REPRESENTING AN IMPORTANT DEFENSE MECHANISM AGAINST TISSUE
INVASION.

CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (potential).

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or send an email to license@isb.sib.ch).

CC EMBL: J04151; AAA26632.1; -
DR InterPro: IPR004237; Fn_bind.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF02986; Fn_bind; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR Pfam: PF04650; Gram_pos_anchor; 1.
DR TIGRPFAMs: TIGR01167; LPTXG_anchor; 1.
DR TIGRPFAMs: TIGR01168; YsIRK_signal; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Repeat; Signal.

FT CHAIN 1 36 FIBRONECTIN-BINDING PROTEIN.
FT PROPEP 37 985 REMOVED BY SORTASE (POTENTIAL).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X APPROXIMATE TANDEN REPEATS,

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FT REPEAT 745 782 FIBRONECTIN-BINDING DOMAIN.
FT REPEAT 783 820 D-1.
FT REPEAT 821 859 D-2.
FT REPEAT 860 878 D-3.
FT REPEAT 879 948 D-4 (INCOMPLETE).
FT REPEAT 879 948 5 X TANDEM REPEATS, PRO-RICH (WR).
FT REPEAT 893 906 WR1.
FT REPEAT 907 920 WR2.
FT REPEAT 921 934 WR3.
FT REPEAT 935 948 WR4.
FT SITE 982 986 LPTXG SORTING SIGNAL (POTENTIAL).
FT MOD_RSS 985 985 AMIDE-LINKED TO CELL WALL (POTENTIAL).
SQ SEQUENCE 1018 AA; 11780 MW; 58175E020E81F1F CRC64;

Query Match 19.1%; Score 331; DB 1; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.1e-11;
Matches 82; Conservative 77; Mismatches 146; Indels 28; Gaps 11;

QY 10 GTDITNCTNTVTVGIDSG---TTVYPHQAGYVLYNGFVSVPNSAVKGFRTKTPKELN 65
DB 194 GTDVTSKVT-VEIGSIEGHNTNTNVEPHAGQRAVLKTKLKFENGLHQDYDFELSNVN 252
QY 66 LNGTSTAKVPPIAAGQOVLANGVIDSDGNTVTFDTYVNTKDYKATLTPAYIDENV 125
DB 253 THGVSTARKVPEIKNGSVVMATGEVLGGKIRYTFNDIEDKVDVTALEINLFIDPKTV 312
QY 126 KKTGVNLTATIGSTTANKTVLDVY-EKYGFYMLSIGITDQDKNTNTYRQTIYVNS 184
DB 313 QTNNGQITSTLNEHQSKELDVYKQIGINY-ANLNGSIEPTNKANRFSHAFIKPN 371
QY 185 GDNVIAPLTGNLKPNTDSNALIDQNTSIKYK-VDNADLSSTYVN---PENEDVT 240
DB 372 NGKTTSTVTVTGLKNGSNQNG---NOPKXRIEFLNGNEDIAKSVANTDTSKFEV 427
QY 241 NSV-NITFPNPNQYKVEFNPDDQITPYIVVNGHIDPNSKGLDLRSTLYGYSNI 238
DB 428 SMSGNLNLQNGGYSLSNI---ENLDITVYVHYDGEV-LNGTDEVPFRQTMVHPQOLY 482
QY 299 -----WRSMGWNEVAFNNGSGGDIKPVV 325
DB 483 KYYYDRGYTLTMDNGLVLYSKNANGNEKNGP 515

RESULT 2
SLAP_ACEKI STANDARD; PRT; 762 AA.
ID SLAP_ACEKI STANDARD; PRT; 762 AA.
AC P22258;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell surface protein precursor (S-layer protein).
OS Acetogenium kivi.
OC Bacteria; Firmicutes; Clostridia; Thermocaeobacteriales;
OC Thermocaeobacteriaceae; Thermocaeobacter.
OX NCBI_TaxID=2325;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DSM 2030;
RX MEDLINE=90036724; PubMed=2681162;
RA Peters J., Peters M., Lotsepelch F., Baumeister W.;
RA Kellermann J., Lotsepelch F., Baumeister W.;
RT "S-layer protein gene of Acetogenium kivi: cloning and expression in Escherichia coli and determination of the nucleotide sequence.";
RL J. Bacteriol. 171:6307-6315(1989).
RN [2]
RP PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
RC STRAIN=DSM 2030;
RX MEDLINE=92281580; PubMed=1596358;
RA Peters J., Rudolf S., Oschkinat H., Mengers R., Sumper M.,
RA Kellermann J., Lotsepelch F., Baumeister W.;
RT "Evidence for tyrosine-linked glycosaminoglycan in a bacterial surface protein.";
RL Biol. Chem. Hoppe-Seyler 373:171-176(1992).

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RN [3]
RP DOMAINS.
RX MEDLINE=94156823; PubMed=8113161;
RA Lupas A., Engelhardt H., Peters J., Santarius U., Volker S.,
RA Baumeister W.;
RT "Domain structure of the Acetogenium kivi surface layer revealed by electron crystallography and sequence analysis.";
RL J. Bacteriol. 176:1224-1233(1994).
CC -1- FUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.
CC -1- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry.
CC -1- PTM: THE CARBOHYDRATE CONTENT OF THIS PROTEIN IS ABOUT 8% WHICH CORRESPOND TO ABOUT 40 TO 50 SUGAR MOLECULES PER MONOMER. O-LINKED GLYCANS CONSIST OF GLC, GALNAc AND GLCNAC.
CC -1- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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CC EMBL: M31069; AAA21930.1; -.
CC PIR: A34355; A34355.
CC InterPro: IPR001119; SLH.
CC Pfam: PF00395; SLH; 2.
CC PROSITE: PS01072; SLH DOMAIN; 2.
CC Signal: Glycoprotein; Repeat; Cell wall; S-layer.
CC CHAIN 1 26
CC DOMAIN 27 762 CELL SURFACE PROTEIN.
CC FT 30 94 SLH 1.
CC FT 95 145 SLH 2.
CC FT 146 204 SLH 3.
CC FT 473 479 SER/THR-RICH.
CC FT 625 630 SER/THR-RICH.
CC FT 297 297 O-LINKED (GLC. . .).
CC FT 516 516 O-LINKED (GLC. . .).
CC FT 520 520 O-LINKED (GLC. . .).
CC FT 632 632 O-LINKED (GLC. . .).
CC CARBOHYD 516 516 O-LINKED (GLC. . .).
CC CARBOHYD 520 520 O-LINKED (GLC. . .).
CC CARBOHYD 632 632 O-LINKED (GLC. . .).
CC SEQUENCE 762 AA; 82785 MW; 34BC9C784DECA67E CRC64;

Query Match 7.4%; Score 129; DB 1; Length 762;
Best Local Similarity 21.6%; Pred. No. 1.1;
Matches 79; Conservative 54; Mismatches 113; Indels 120; Gaps 19;

QY 15 NQITNTVTVGIDG-GTTPYPHQAGYVLYNGFVSVPNSAVKGFRTKTPKELN---LNG- 68
DB 280 NDVVSFTQGDSDVGTVTV-----KNDNKAIAIKVDVAAYLVLYNGY 319
QY 69 VNSTAKVP-----PIAAGQOVLANGVIDSDG---NVYTFPTDYVN--TKDVKATILM 116
DB 320 LTVSKYTYKGAQVITIIINNVILVNGSYDNTIYVNVQSDKYLINDSNELKGTIV 379
QY 117 PAYIDENVKKTGNVTLATIGSTTANKTVLDVYERYKGFVNS-----IK 162
DB 380 -----TGAVSKVTDI---KAN-----DYVYGGQYDVGNGVGTVIYVNVQVT 420
QY 163 GTIDQDKNTNTYRQTIYVNSGDNVIAVLNGN---LKPNDSNALIDQNTSIKYK 218
DB 421 GITEKSVGSQSTYKASI-----DNVSYVADNNVANGLEPKKTVIILKNVIVGI-- 472
QY 219 VDNADLSSTYVNPENFEDVTVNSVNIITPENQYKVEFNPDP-----DQI 264
DB 473 -----SSTTTTAVNVAIFKESDPTAWPA-----KVKLILDAEKVDAVYSDVYDKV 523
QY 265 TTYIYIVVANGHIDPNSK-----GDLARSTLYGNSNIIRMSG---WDNEVAFNNG 313
DB 524 NLAEGITVIVYVANGKLANDIQRANQDPSSASYSKADAKVLTREGSTTYITITNVLINNT 583
QY 314 SSGSDG 319

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Db 810 LRVGGVKSNTNLTNDSAVTFPTNPVVTGAIDNTGNANGIVTFTGDSVTGNIGNT 869
 QY 187 NVIAVPLTGNLKPNTDSNALIDQONTSIKVKYKVNMAADLSSEYFVNEFEDVTSVNIT 246
 Db 870 NALATISGAKKA-TLGGAIITKATTTKLT---TNASAVT---FTNP---VVVTGAIDNT 918
 QY 247 FPNPQYKVEBNTPDQDIT---TPYIVVN-----GHIDPSKDDLRLSTL 290
 Db 919 -GNANGIVTF-TGDSVTGNIGNTNALTATVAGVTLQAGSGSLDANNI-DFGARSTL 974

RESULT 4

ID FLID_CAMBJE STANDARD; PRT; 642 AA.
 AC Q9PRW6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Flagellar hook-associated protein 2 (HAP2) (Filament cap protein)
 DE (Flagellar cap protein).
 GN FLID OR C00548.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteriaceae; Campylobacter.
 OX NCBI_TaxId=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCCTC 11168;
 RX MEDLINE=20150912; PubMed=10688204; Kestley J.M., Churcher C.,
 RA Parkhill J., Wren B.W., Mungall K., Kestley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtcycd S.,
 RA Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.,
 RA "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences";
 RT Nature 403:665-668(2000).
 RL Nature 403:665-668(2000).
 CC -1- FUNCTION: REQUIRED FOR THE MORPHOGENESIS AND FOR THE ELONGATION OF
 CC THE FLAGELLAR FILAMENT BY FACILITATING POLYMERIZATION OF THE
 CC FLAGELLIN MONOMERS AT THE TIP OF GROWING FILAMENT. FORMS A CAPPING
 CC STRUCTURE, WHICH PREVENTS FLAGELLIN SUBUNITS (TRANSPORTED THROUGH
 CC THE CENTRAL CHANNEL OF THE FLAGELLUM) FROM LEAKING OUT WITHOUT
 CC POLYMERIZATION AT THE DISTAL END (BY SIMILARITY).
 CC -1- SUBUNIT: Homopentamer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Flagellar.
 CC -1- SIMILARITY: Belongs to the flid family.
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 CC
 CC EMBL: A139075; CAB75184.1; -.
 DR PIR: D81401; D81401.
 DR InterPro: IPR003481; FLID.
 DR Pfam: PF02465; FLID; 1.
 DR Flagellum; Coiled coil; Complete proteome.
 KM DOMAIN 614 641 COILED COIL (POTENTIAL).
 SO SEQUENCE 642 AA; 69775 MW; 40FF20D41688EEA3 CRC64;

Query Match 7.3%; Score 127; DB 1; Length 642;
 Best Local Similarity 20.9%; Pred. No. 1.1; Indels 142; Gaps 19;
 Matches 86; Conservative 48; Mismatches 136;
 QY 21 TVGIDSGTIVYPPHAGVYKLVNG---FSVPSAVVAGDFTFKITV-PKEINLNGVSTAKY 75
 Db 146 TVTVVDKNTT-YRLADKINAGSGEIVAKIVNGEGTGYRLTLTSGETGDSALS----- 200
 QY 76 PTMAGDQVLANGVSDGAVITFTDYNTVDQVAKLTMPYIDPENVKR----- 127

Db 201 --FYAKGD-SNGKXKXKINAEKIF-----DLGWLGLDVASIDPDKCKKGYGKINDAS 250
 QY 128 -----TGAVTLANGIGST-TANTVTVLDVYKAKGKFNLSIKGTID 166
 Db 251 LHIQTANNAEFTLDGKMKFRSSNTVTDVGWTLTLNKTGELNFDVQDFEGVT-KAMQD 309
 QY 167 QIDKTN---NTYRQIY-----VAPSGDNVIAVPLTGNLKPNTDSNALI 207
 Db 310 LVDAYVDVLTNMAATDYNSETGTGTLQGISVNSISSLIADLPDQVYDGTEDANG 369
 QY 208 DQONTSIKV-----YKVDNADLSSEYFVNEFEDVT-----TPYIVV 271
 Db 370 NKVNTKVMLSMODFGSLNDAGTLSDSSKRPQKVEDPDSIESFFSNITKXEDINHGE 429
 QY 241 -----NSVNIFFPNQYKVEBNTPDQDIT-----TPYIVV 271
 Db 430 VIKTGSLSKYLNSNGNITGLER-KPGDPTIVFNQYTDLSNSDQTNFKLTGKEEBEL 488
 QY 272 VN--GHIDPSKDDLRLSTLTVGYNSNIIRMSWDNEVAFN--NGSGSGD 318
 Db 489 QNLANH--NSKQIEGLKVKVESYNQ-----NTGFRILNPSGDGSSD 529

RESULT 5

ID OMPA_RICRI STANDARD; PRT; 2249 AA.
 AC P1592;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
 DE antigen) (rOmpA) (rOmp A).
 GN OMPA.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxId=783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R;
 RX MEDLINE=90354033; PubMed=2117568;
 RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.,
 RT "A protective protein antigen of Rickettsia rickettsii has tandemly
 RT repeated, near-identical sequences";
 RT Infect. Immun. 58:2760-2769(1990).
 RL Infect. Immun. 58:2760-2769(1990).
 CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
 CC -1- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
 CC layer with hexagonal symmetry.
 CC -1- PTM: Glycosylated (Probable).
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPA FAMILY.
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 CC
 CC EMBL: M31227; AAA26380.1; -.
 DR PIR: A41477; A41477.
 DR InterPro: IPR006315; Autotransport.
 DR InterPro: IPR005546; Autotransporter.
 DR Pfam: PF03797; Autotransporter; 1.
 DR TIGRfams: TIGR01414; autotransp_bar1_3.
 DR Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
 KM SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
 FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 212 286 A (TYPE I).
 FT REPEAT 287 358 B (TYPE II).
 FT REPEAT 359 430 C (TYPE II).
 FT REPEAT 431 505 D (TYPE I).

FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 578 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C085DF087 CRC64;

Query Match 7.0%; Score 121.5; DB 1; Length 2249;
Best Local Similarity 22.3%; Pred. No. 12;
Matches 78; Conservative 38; Mismatches 144; Indels 89; Gaps 14;

QY 14 TNOITNVVG-----IDSGTIVPHQAGYKLVNGFSVPSA---GDTFKIT 59
DB 878 TNSLATISVAGATATLGAIVKATTKLTNAASVLTITNANAVLTGALDNTTGGDNVGV- 936
QY 60 VPKEINLVG-----TSTAKVPIVAGDQVLANGVIDSDGNVYTFEDVYNTKD 109
DB 997 ---LNLGALASQVAGDIGNTSLATISVAGATLGAIVKA-----TTTKLTDAASA 986
QY 110 VKAT--LTMFAVIDPEN-----YKKTGVLTATIGSTTANKYV----- 146
DB 987 VKFTIPVAVTGAIDVTGNANNGIVFTGNSVTGVNVTNATVAGAGLLQVGGVVK 1046
QY 147 ---LVDEKKGKRYN-LSIKGTIDQIDKTN-----TYRQIYVNSGDNVIAVLTG 195
DB 1047 ANTILTLTNDASAVTTPNPVVTGALDNTGNANNGIVTGTGNTGVNVTNATVAG 1106
QY 196 NIKENTSNALIDQONTSIKRYKVNAADLSSEYVNP-----ENFEDVTSVNTFFP 248
DB 1107 ---AGLLQVGGVVKANTINLTNDASAVTTPNPVVTGALDNTGNANNGI-VTFT 1157
QY 249 NPNQYKVENPTDDQITTFYIVVNGHIDPNKGPALRSTLYGNSNI 297
DB 1158 GNSVTGTGIGNTALAT---VVGAGITLQAGSSLAANNIDFGARSTL 1202

RESULT 6
DNAA_OCEIH STANDARD; PRT; 612 AA.

ID DNAA_OCEIH
AC O8BPM4:
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chapterone protein dnak (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
GN DNAA OR O81968.
OS Oceanobacillus theyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
CC NCBI_TaxId=182710;
RN SEQUENCE FROM N.A.
RX STRAIN=HTE831 / DSM 14371 / JCM 11309;
RC MEDLINE=2220767; PubMed=1235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus theyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."
RT Nucleic Acids Res. 30:3927-3935(2002).
CC -1- FUNCTION: Acts as a chaperone (By similarity).
CC -1- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
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CC -----
DB EMBL; AP004599; BAC13924.1; --
DR HAMAP; MF_00332; --1
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PRO0301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KM Chapterone; ATP-binding; Heat shock; Phosphorylation;
KW Complete proteome.
FT MOD RRS 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT SEQUENCE 612 AA; 66558 MW; 5097482DC007BB41 CRC64;

Query Match 7.0%; Score 120.5; DB 1; Length 612;
Best Local Similarity 20.7%; Pred. No. 2.6;
Matches 77; Conservative 54; Mismatches 106; Indels 135; Gaps 20;

QY 22 VGIDSGTT-----YYPH-----QAGYKLVNTGFSVPS- 49
DB 5 IGIDLTGNSCVSMGEBAVVPNPNENRTSPSVAFKNGEROYGEVAKROAITNPNT 64
QY 50 -AYK---GDTFKITV-----PKELN---LNGVSTAKVPIVAGDQVLANGVIDSDGNV 96
DB 65 QSIKRMHGDYKRYKIEKRYTPOEVSAILIQYKSYAE----- 102
QY 97 IYTFDYVNTKDVKATLTMFAVI---DPENYKKTGNV-----TATGIG 138
DB 103 ---DYIGKXVE-KAVITVPAFYNDARQATDACKIAGLEVERIINEPTAAALAYGID 156
QY 139 STANKKVLVDYKKGKRYNLSIKGTIDQIDKTNNTYRQIYVNSGDNVIAVLTG 198
DB 157 KEDDQDITLV-YDLGGTFEVS-----LDIGDGFEE--VVTAGDN-----RIG 198
QY 199 PNTDSNALIDQONTSIKRYKVNAADLSSEYVNPENFEDVTSVNTFFPNQYKVEN 258
DB 199 GDEPDQYITDM---VQEPKKNALIDSDQKAT-QRLDAAKAKKADLSGVTV----- 248
QY 259 TPDDQITTFYIVVNGHIDPNKGPALRSTLY-----GNSYIIRKSMWNEVAFNNG 313
DB 249 ---TQISLPRTIA-----GDAGPLHLEMTMSRAKFDLSLVVERTVQ-PTRKALSDA 297
QY 314 SSGSGDIDKPEV 325
DB 298 SLKSDIDKXVL 309

RESULT 7

GP10_DICDI STANDARD; PRT; 544 AA.

ID GP10_DICDI
AC O06885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Glycoprotein gp100 precursor (P29F8).
GN GP1A.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
CC NCBI_TaxId=44689;
RN SEQUENCE FROM N.A.
RX MEDLINE=94124612; PubMed=8294503;
RA Barth A., Mueller-Taubenberg A., Taranto P., Gerisch G.;
RT "Replacement of the phospholipid-anchor in the contact site A glycoprotein of D. discoideum by a transmembrane region does not impede cell adhesion but reduces residence time on the cell surface."
RT J. Cell Biol. 124:205-215(1994).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DEVELOPMENTAL STAGE: Restricted to the aggregation stage of development in D. discoideum. No detectable activity in cell

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CC      adhesion.
CC      -1- PTM: N- and O-glycosylated.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: 104286; AAC37369.1; -
DR      DictyBase; DDB0001546; GPDA.
KM      Glycoprotein; Transmembrane; Signal.
FT      SIGNAL 1 19
FT      CHAIN 20 544
FT      DOMAIN 20 489
FT      TRANSMEM 490 510
FT      DOMAIN 511 544
FT      DOMAIN 117 208
FT      CARBOHYD 80 80
FT      CARBOHYD 224 224
FT      CARBOHYD 308 308
FT      CARBOHYD 332 332
FT      CARBOHYD 366 366
FT      CARBOHYD 380 380
FT      CARBOHYD 410 410
FT      CARBOHYD 422 422
FT      CARBOHYD 478 478
SQ      SEQUENCE 544 AA; 59156 MW; 9B2C2CE7C7D0DA0 CR664;

Query Match 6.9%; Score 119.5; DB 1; Length 544;
Best Local Similarity 20.3%; Pred. No. 2.6;
Matches 70; Conservative 47; Mismatches 104; Indels 123; Gaps 16;

QY 11 TDTIT-QLNVTWYIGISGTTVPHQGYKLVKNGFVSAPNAKGVDFKTKVKEKLNKV 69
DB 226 TDIEDIEMGKITTSYKNGOSSSR-----FQPSNLIK-----SI 259
QY 70 TSTAKYPPIMAGQVLAVGVIDSQNVITFTDYVNTKDVKATLTPAYIDPENVKCTG 129
DB 260 ERINSV-----CGVTEPKGSFFY-----DDYERSI-----KITG 288
QY 130 NVTLAGISGTANKVTVVVEYKFKFYNLSIKGTDIDDKNTYKQITVYVNSGDVNI 169
DB 289 NKICETLTSSQTSIRCYLTNGTGG--YTTIDNLINPDNNNSNLTYCYANPIIDKVI 346
QY 190 A-----PVLITGNL-----KENTD-----SNALIDQONTIKYKVDNAADSE 227
DB 347 GYMDKULTITTIICKFNINATVIEKPNKNGKNCNSVALSTDTLFI-----CELSK 398
QY 228 SYFV--NPNEDVTVSVNTTFPNQCYKFEVTPDQITTPITVYVNGHI----- 276
DB 399 SYHTLSSPK-----TTNTTMLSFIN-----NSPSTVSENIETMISGFQIKISTKDS 446
QY 277 ---DPSKQGLALSTLYGYSNINIMRSMGMDNEVAFNNSGSG 317
DB 447 TTDDNNKNNDDGSEIDSVKSAVDSKS-----NNNSGGG 483

RESULT 8
ALIE7_AZOVI STANDARD; PRT; 856 AA.
AC Q9R9G9;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poly(beta-D-mannuronate) C5 epimerase 7 (EC 5.1.3.-) (Mannuronan
DE epimerase 7).
DE ALG67.
OS Azotobacter vinelandii.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OS Pseudomonadaceae; Azotobacter.
OR NCBI_TaxID=354;
RX [1]
RX SEQUENCE FROM N.A.
RP STRAIN=E;
RX MEDLINE=99084941; PubMed=9864314;
RX Svane B.I.G., Skjaek-Braek G., Ertesvaag H., Valla S.;
RT "Cloning and expression of three new Azotobacter vinelandii genes
RT closely related to a previously described gene family encoding
RT mannuronan C-5-epimerases."
RL J. Bacteriol. 181:68-77(1999).
RN [2]
RN EXPRESSION.
RP STRAIN=E;
RX MEDLINE=21132699; PubMed=11243259;
RX Hoeidel H.K., Glaerum Svane B.I., Gimmedstad M., Valla S.;
RT "Mannuronan C-5 epimerases and cellular differentiation of
RT Azotobacter vinelandii."
RL Environ. Microbiol. 2:27-38(2000).
RN [3]
RN CHARACTERIZATION, AND MUTAGENESIS OF ASP-152.
RP STRAIN=E;
RX MEDLINE=21402877; PubMed=11390391;
RX Glaerum Svane B.I., Strand W.I., Ertesvaag H., Skjaek-Braek G.,
RX Hartmann M., Barbeyron T., Valla S.;
RT "The catalytic activities of the bifunctional Azotobacter vinelandii
RT mannuronan C-5-epimerase and alginate lyase Alg7 probably originate
RT from the same active site in the enzyme."
RL J. Biol. Chem. 276:31542-31550(2001).
RN [4]
RN REVIEW.
RP MEDLINE=20391728; PubMed=10937941;
RX Ertesvaag H., Hoeidel H.K., Schjerve H., Glaerum Svane B.I.,
RX Valla S.;
RT "Mannuronan C-5-epimerases and their application for in vitro and in
RT vivo design of new alginates useful in biotechnology."
RL Metab. Eng. 1:262-269(1999).
CC -1- FUNCTION: Converts beta-D-mannuronic acid (M) to alpha-L-gulonic
CC acid (G). Has both epimerase and lyase activities. Contributes to
CC abortive encystment by degrading the coat from inside the cyst.
CC Important for cyst germination.
CC -1- COFACTOR: Calcium.
CC -1- ENZYME REGULATION: Inhibited by zinc.
CC -1- PATHWAY: Alginate biosynthesis.
CC -1- SUBCELLULAR LOCATION: Extracellular. Probably exported via the
CC hemolysin-type secretion pathway.
CC -1- DEVELOPMENTAL STAGE: Produced mainly in germinating cells.
CC -1- DOMAIN: Composed of one catalytically active A module and three R
CC modules.
CC -1- MISCELLANEOUS: Each enzyme of this family of C5 epimerases
CC introduces its own characteristic sequence distribution of G-
CC blocks in their substrates, explaining the extensive sequence
CC variability of alginates. These alginates of varying composition
CC have different physical properties and are necessary at different
CC stages of the bacterium life cycle.
CC -1- SIMILARITY: belongs to the D-mannuronate C5-epimerase family.
CC -1- SIMILARITY: Contains 8 hemolysin-type calcium-binding repeats.
CC -1- SIMILARITY: Contains 9 Pbl1 repeats.
CC -----
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CC -----
CC EMBL: AF099800; AAD04921.1; -
DR InterPro; IPR006633; CASH.
DR InterPro; IPR001343; HemIyan_Ca_bind.
DR InterPro; IPR006626; Pbl1.
DR Pfam; PF00353; hemolysinCbind; 8.
DR PRINTS; PR00313; CASHNDNRPRT.
DR SMART; SM00722; CASH; 2.
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DR SMART; SMO0710; PBH1; 9.
DR PROSITE; PS00330; HEMOLYSIN CALCIIUM; 6.
KM Arginase biosynthesis; Isomerase; Calcium; Repeat; Multigene family.
FT REPEAT 133 155
FT REPEAT 157 179
FT REPEAT 180 202
FT REPEAT 204 226
FT REPEAT 234 256
FT REPEAT 257 279
FT REPEAT 280 304
FT REPEAT 320 342
FT REPEAT 386 403
FT REPEAT 404 421
FT REPEAT 422 439
FT REPEAT 537 554
FT REPEAT 555 572
FT REPEAT 573 590
FT REPEAT 714 731
FT REPEAT 732 749
FT MUTAGEN 152
SQ SEQUENCE 856 AA; 90364 MW; 626DDCA4681E8607 CRC64;
Query Match 6.8%; Score 117; DB 1; Length 856;
Best Local Similarity 21.8%; Pred. No. 6.6; Indels 116; Gaps 20;
Matches 82; Conservative 52; Mismatches 127;
QY 8 AAGTDTNLTNTVTVGIDSGTYVPHQAGYVKLVNCFSPNSAVKADTFKITVPEKLNIN 67
Db ADGTDVTS-IGNSV---SGT-----QRIYQLS-CTNSTFGSRSDAVQF-----ID 386
QY 68 GVTSTAKV-PPM-----AGDOVLANG-----VIDSGNVITTTD--- 102
Db GSTGNDLITGTPADIIVGSGNDLTSGDANDVLEGAGSDRLTGGEGADIFRTAVSD 446
QY 103 --VYNTKDVKATLTPAYIDPENVKKTGNTLATIGSTTA-----NKTVLVDYEX- 152
Db 447 SYTTASSVADQILDPSADNRIDLTGLGFTGLSDGCGTLAVLANSQSRITLASYED 506
QY 153 -YGFYNLSIKGT-IDQIDXTNNTYQITVYVPSGD---NVIAPVLTKNKEMTDS-- 203
Db 507 ADGRYSLTLDGNFVGRRLDSDNLVFRKTIAGTEGDSLTGNAMAEIILDG--SGNDSIA 564
QY 204 -----NALIDQNTS-----IKVYVNDAAADLSBEYFNPENFEDVNTS 242
Db 565 GGLGNDLVLRGAGDDILNGGLGSDQSLGGBGADIFRTSVAD--SYQNSGDNFSDLT-- 619
QY 243 VNITFENQYKVEFNTPDQITTPYIVVNGHIIDNSKGLDALRSTIYGYSNNIWRSM 302
Db 620 -----LDFPGEDR-----IDLSGLGFGSLGD--GHNGTILLMTS 652
QY 303 SWDNEVAFNNGSGSGDG 319
Db 653 SETNRTYLNKFPDADG 669

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RX MEDLINE=99081766; PubMed=9864239;
RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
RT "Identification of two novel genes encoding 97- to 99-kilodalton outer
RL membrane proteins of Chlamydia pneumoniae.";
RL Infect. Immun. 67:375-383(1999).
[2]
RX STRAIN=VR1310;
RC MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RL role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
[3]
RX STRAIN=CWL029;
RC MEDLINE=99206606; PubMed=10192388;
RA Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S., Trachomatis.",
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
[4]
RX STRAIN=AR39;
RC MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uitterlind T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Lihner M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RL pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
[5]
RX STRAIN=J138;
RC MEDLINE=20330349; PubMed=10871362;
RA Shiba T., Ishii K., Hattori M., Kubara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RL from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
[6]
RX STRAIN=TW-183;
RC Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RL other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
CC (potential).
CC -1- SIMILARITY: Belongs to the PMP outer membrane protein family.
CC -----
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CC -----
DR EMBL; AJ001311; CA04672.1; -
DR EMBL; AJ13034; CAB37072.1; -
DR EMBL; AE001628; AAD18593.1; -
DR EMBL; AE002192; AAF38159.1; ALT_INIT.
DR EMBL; AP002546; BAA98658.1; -
DR EMBL; AE017158; AAP86399.1; -
DR PIR; D72077; D72077.
DR PIR; H86546; H86546.
DR PHCI-ZDPAGE; O86164; -.
DR TIGR; CP0302; -.

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DR InterPro: IPR003368; Chlamydia_PMP.
 DR InterPro: IPR000437; Prok_lipoprot_S.
 DR Pfam: PF02415; Chlamydia_PMP; 2.
 DR TIGRFAMs: TIGR01376; POME_repeat; 6.
 DR Outer membrane; Signal; Multigene family; Complete proteome.
 FM SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 928 PROBABLE OUTER MEMBRANE PROTEIN PMP11.
 SQ SEQUENCE 928 AA; 98903 MW; 788BCDD62C911402 CRC64;
 Query Match 6.7%; Score 115.5; DB 1; Length 928;
 Best Local Similarity 19.3%; Pred. No. 9.1; Indels 121; Gaps 14;
 Matches 73; Conservative 48; Mismatches 137; Indels 121; Gaps 14;
 QY 22 VGIDSGTIVYPHQAGYKLVNYSFVNSAV-----KGDFTKIVPKELNNGVSTA 73
 DB LGWDSGTTSTAGSITITNLGINVSLGKOPVSLTAGSNKVIYSGKMLIDIEGNI 518
 QY 74 KVPPIAGQOV--LANGVIDSDGNVYTFDYNTKDYKATLTTPAYIDP----- 123
 DB YESHMFSDQLFSLKLTVDAD-----VDINVDISSLPVPAE--DPNSEYFQSQ 567
 QY 124 -----NVKKTGNVTLATIGSTTANKTVLVYERKGFYMLSIKGTIDIDKTN 172
 DB 568 KVVNMTTDAATNKADATWTKTGFVSPERSALVCNTLWGVTDIRSLQQLVEIGATG 627
 QY 173 NTRQITIV-----NPSGDNVAPVLTGNLKP----- 199
 DB 628 MEHQGFVWSSMTNPLHKTGDENRKGFRTSGGYVG---GSAMTPKQDLTFPACHLF 683
 QY 200 NIDSNALIDQONTSIKYKYKNADADSESYFVNPENF-----EDVTNVTNITFPNP 250
 DB 684 ARKDCDIANNNS--RTY--GGLFPKHSHTLPQVYVLLGRKXFESEAIKFPRIPIA 739
 QY 251 NQYKVEPNTDDQITPYIVVNGHIDPNSKDLALRSLTYGNSNITRSMWDNEVAF 310
 DB 740 LDQVQSFHSDNMEHTYSL-----PESSEG-----SWSNECT- 772
 QY 311 NNGSGSGDGIDKPVPEQP 329
 DB 773 ----AGSIGLDLPVLSNP 787

RESULT 10
 OMPB_RICPR STANDARD; PRT; 1643 AA.
 AC 053020; 09ZCMQ;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)
 DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (rmpB)
 DE (Comp B) [Contains: 120 kDa surface-exposed protein (Surface protein
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
 GN OMPB OR SPAP OR SPA OR RPT04.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 NC NCB1_Taxid=782;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC STRAIN=Breini;
 RX MEDLINE=9104597; PubMed=2122457;
 RA Carl M., Dobson M.E., Ching W.M., Dasch G.A.;
 RT "Characterization of the gene encoding the protective paracrystalline-
 RT surface-layer protein of Rickettsia prowazekii: presence of a
 RT truncated identical homolog in Rickettsia typhi";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Breini;
 RA Moron C.G., Yu X.J., Walker D.H.;
 RT "Sequence analysis of ompB of Rickettsia prowazekii";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria";
 RL Nature 396:133-140(1998).
 RN [4]
 RP PARTIAL SEQUENCE.
 RC STRAIN=Breini;
 RX MEDLINE=92114896; PubMed=1370573;
 RA Ching W.M., Carl M., Dasch G.A.;
 RT "Mapping of monoclonal antibody binding sites on CNB fragments of
 RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
 RT prowazekii";
 RL Mol. Immunol. 29:95-105(1992).
 RN [5]
 RP CLEAVAGE SITE.
 RX MEDLINE=92104668; PubMed=1729180;
 RA Hackstadt T., Messer R., Cieplak W. Jr., Peacock M.G.;
 RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
 RT membrane protein of rickettsiae: identification of an avirulent mutant
 RT deficient in processing";
 RL Infect. Immun. 60:159-165(1992).
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
 CC -1- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
 CC layer with hexagonal symmetry.
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
 CC -----
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 CC -----
 DR EMBL: M37647; AAA26390.1; ALT_INIT.
 DR EMBL: AF161079; AAD42234.1; -.
 DR EMBL: AJ235273; CAAL5140.1; -.
 DR PIR: D71630; D71630.
 DR InterPro: IPR005546; Autotransporter.
 DR InterPro: IPR006315; Autotransporter.
 DR Pfam: PF03797; Autotransporter; 1.
 DR TIGRFAMs: TIGR01414; autotrans_bar1; 2.
 KW Antigen; S-layer; Cell wall; Complete proteome.
 FT CHAIN 1 1328 120 KDA SURFACE-EXPOSED PROTEIN.
 FT CHAIN 1 1328 32 KDA BETA PEPTIDE.
 FT VARIANT 257 257 V -> A (IN STRAIN BREINI).
 FT VARIANT 1010 1010 Y -> D (IN STRAIN BREINI).
 FT VARIANT 1450 1450 A -> S (IN STRAIN BREINI).
 FT CONFLICT 178 179 AA -> VC (IN REF. 1).
 FT CONFLICT 191 201 TTQAPLPLGA -> INSRSSVHLVS (IN REF. 1).
 FT CONFLICT 212 212 T -> I (IN REF. 1).
 FT CONFLICT 313 313 Q -> L (IN REF. 1).
 FT CONFLICT 1104 1104 D -> G (IN REF. 2).
 FT CONFLICT 1123 1123 T -> S (IN REF. 2).
 SQ SEQUENCE 1643 AA; 169855 MW; 735FDF392B6346CC CRC64;
 Query Match 6.6%; Score 114.5; DB 1; Length 1643;
 Best Local Similarity 21.0%; Pred. No. 22;
 Matches 80; Conservative 48; Mismatches 140; Indels 113; Gaps 17;
 QY 8 AAGDITNQLNVT---VGIDSGTIVYPHQAGYKLVNYSFVNSAVKG---DFFKIVTP 61
 DB 127 AAG-----KIINTGGITVOEASNTINQVALTKHGAAINANDSLGSGITF-AAAP 180

QY 62 KELINGVTSTAKVPIMAGDOVLANGVIDSDGNVYFTD-VYNTKDVATL----- 114
DB 181 SVLERNLINPTIOEAPLTIG-----ANSKIYNGNGNTLNTNGFIQVSDTFFGITTIND 236
QY 115 -----TMPAYIDPENVKKTGNVTLATIGSTANKTVLDYERKGFYNSIKGTID 166
DB 237 DCGJWFENSTPDPAANTLNLQVGNTINFGIDGT--GKLVY--SKNGAATFEFNTGTL- 291
QY 167 QIDKNTNTKQITLVNPSGDNYAPLTENLKNPDSNA--LIIDQNSIKYKTDNAD 224
DB 292 -----GDN-----LKGILNTAAVAGKLIISOGAANAATGTDDNGG 328
QY 225 LBSYFVNEP-----NFEDVTSV 243
DB 329 RAAGFIVSDNGMAATISGQVYAKMVIQSANAGGVTEPHIVDGLGGTFNFKTADSKV 388
QY 244 NTFEPNPGYKFEFTPDQITPTIYVYNGHI--DPNSKDLALSTLYGNSNITMRS 301
DB 389 IIT-ENSNFGSTNFGNLDQIVVPDPTKILKNFIDGVKNNGTA--GVITENANGALVS 444
QY 302 MSWNEVAFNN-----GSGSG 317
DB 445 ASTDPNIAVTNINAIABEGAG 465
RESULT 11
Y013_BPL2 STANDARD; PRT; 738 AA.
ID P42548;
AC 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Hypochemical 81.3 kDa protein precursor (ORF13).
OS Bacteriophage L2.
OC Viruses; dsDNA viruses, no RNA stage; Plasmaviridae; Plasmavirus.
NCBI_TaxID:46014;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94215869; PubMed=8163159;
RA Maniloff J., Kampo G.J., Dascher C.C.;
RT "Sequence analysis of a unique temperature phase: mycoplasma virus
L2."
RL Gene 141:1-8(1994).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L13696; AAA87969.1; -
KW Hypochemical protein; Signal; Transmembrane.
FT SIGNAL 1 27
FT CHAIN 28 738 HYPOTHETICAL 81.3 kDa PROTEIN.
FT TRANSMEM 612 632 POTENTIAL.
FT TRANSMEM 712 732 POTENTIAL.
SQ SEQUENCE 738 AA; 81312 MW; 87479A3267C89646 CRC64;
Query Match 6.6%; Score 114; DB 1; Length 738;
Best Local Similarity 22.4%; Pred. No. 8.3;
Matches 75; Conservative 50; Mismatches 110; Indels 100; Gaps 19;
QY 41 NNGSGVNSAVKGDFTKITPKELNNGVSTAKVPIMAGDOV--LANGVDS---DGN 95
DB 420 NDGSGPVTGIVNVEFSVT-----NSNGQTSI-LAPVHVVDVNPVINSVDTVHISYD 473
QY 96 VIYTFDVTYNTKDVKATLTPAYIDPENVKKTGNVTLATIGSTANKTVLDYERKGF 155
DB 474 QTFNVNTWNS-----LTVSDNY-----TGLSISIKENTYVNTNKKLGI 513

QY 156 FYNLSIKGTIDQIDKTN--TYRQITVNP-----SGDNVAPVLTGN----- 196
DB 514 Y-----KIYGAVDPSGNIGTLRTIVNDGIGPVPNGINTIYASINENITVYQIKAGLA 568
QY 197 -----LKPNTSNALIDQON-----TSIKYK-----VDNAAD-----LBSYFVNEPNE 237
DB 569 AIDAIDGNVTTISIVDSNLTGRANTGVYEVFRAVDAAGNQTFFHTVVISIVASPPGF 628
QY 238 DV-TNSVNIETPNP-----QYKVEFTPD-DQITPTIYVYNGHIIDPNSKDLALSTLY 291
DB 629 IINNSVRL-LPGANLTIHQILNINASDAENSTNYTSVPQTYN-----LSFTLY 679
QY 292 GYNSNIIRMSMDNEVAFNNGSGSGDGDIDKPYVP 326
DB 680 GESHQVSIYVAGNDSI-----IPTPIVP 703
RESULT 12
SLAP_BACST STANDARD; PRT; 1228 AA.
ID P35825;
AC 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DS S-layer protein precursor (Surface layer protein).
GN SBA.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID:1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PV72;
RX MEDLINE=94320770; PubMed=8045409;
RA Kuen B., Sleytr U.B., Lubitz W.;
RT "Sequence analysis of the sba gene encoding the 130-kDa
RT surface-layer protein of Bacillus stearothermophilus strain PV72."
RL Gene 145:115-120(1994).
CC -1- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC of proteins which coat the surface of bacteria.
CC -1- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
CC layer with hexagonal symmetry.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X71092; CA850409.1; -
DR EMBL; AX000218; CA877069.1; -
DR PIR; I40468; I40468.
KW Signal; Cell wall; S-layer.
FT SIGNAL 1 30
FT CHAIN 31 1228 S-LAYER PROTEIN.
SQ SEQUENCE 1228 AA; 131076 MW; 9F1383AD810C0B0F CRC64;
Query Match 6.6%; Score 113.5; DB 1; Length 1228;
Best Local Similarity 22.1%; Pred. No. 17;
Matches 90; Conservative 51; Mismatches 139; Indels 127; Gaps 24;
QY 12 DITNQLNNTVG-----IDSGTTYPH-----QAGYKLVNGFSV--PNS 49
DB 769 DAVTLTVNDAGQFTIQFSEELKTSGLGKATVEKLNNMGVAVAGTIVSVAKPT 828
QY 50 AVKGDFTKITPKELNNGVSTAKVPPI-MAGQVVLANGVIDSDGNV-----YFTD 102
DB 829 DANG--KVTA-AVTTLTGLNNDKADKRLVVDKSSSTDGIADVAAGVYKEDILIRNS 884
QY 103 YVNT-----KDVKATLTP-----AYIDPENV-----KKTGN 130
DB 885 WHTIVASVKAADKQGAASAFAFTSTADITTKSLVFNSTDLAEVPEFNIIVKDAAGN 944

QY 131 VTLATGI---GSTTANKTVLVDE--KYGKFNLSIKGTIDQDKTNNY---RQTIYVN 182
 DB 945 AVAGTVALDGSF--NKFVFTSQELKAGTVSVITDGRDKNGNLSIKTISFKTVSAN 1002
 QY 183 PGSDNVIAPVLTONLKPNTDSNALIDQ-----NTSIKYKYNADLSSESIPVNPENF 236
 DB 1003 PT---LSSISLADGAVNDRSKTITIEFSDSVNPITLTKADG----- 1043
 QY 237 EDVTSNVNITFPNPQ---YKVEFN---TPDDQITPYIVVNGHI---DPNSK--- 281
 DB 1044 ---TSTNTYVLVANNENKTKYKVFHKGTLDG--FTQYELAVSKPFGCTIDSKVTFI 1098
 QY 282 -GLA---LRSTLYGINSNITFRSMGNDNEVAFNNGSGSGDIDKPV 324
 DB 1099 TGSVAATDEVKPAVLVGGS---WNGTSTYQDPAATRLRSVADFAVEPV 1142

RESULT 13

YFAL_ECOLI STANDARD; PRT; 1250 AA.
 AC P45508; P39441; P45506; P45507; P76468; P77487;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yfal precursor.
 GN YFAL OR B2233.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxId=562;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; Pubmed=9278503;
 RA Blatner F.R., Plunkett G., Ili, Bloch C.A., Perma N.T., Burland V.,
 RA Riley M., Colado-Vides J., Glaeser J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RT Science 277:1453-1474(1997).
 RL
 RN
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97349980; Pubmed=9205837;
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
 RA Ohnita T., Oyama S., Saito N., Samped G., Satoh Y., Sivasundaram S.,
 RA Yamagata S., Horinouchi T.,
 RA Yamagata S., Horinouchi T.,
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT K-12 genome corresponding to 5.0-6.8 min on the linkage map and
 RT analysis of its sequence features.";
 RT DNA Res. 4:91-113(1997).
 RL
 RN
 RN PRELIMINARY SEQUENCE OF 1-938 FROM N.A.
 RX MEDLINE=84272624; Pubmed=6087316;
 RA Carlson J., Fuchs J.A., Messing J.;
 RT "Primary structure of the Escherichia coli ribonucleoside diphosphate
 RT reductase operon.";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:4294-4297(1984).
 RL
 RN
 RN SEQUENCE OF 925-1198 FROM N.A.
 RC STRAIN=K12 / EMG2;
 RA Bester P., O'Keefe T., Robison K., Church G.M.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE OF 1180-1250 FROM N.A.
 RC STRAIN=OV6;
 RX MEDLINE=88201664; Pubmed=2834621;
 RA Hussain K., Elliott E.J., Saimond G.P.C.;
 RT "The pard- mutant of Escherichia coli also carries a gyrAa mutation."

RT The complete sequence of gyrA.";
 RL Mol. Microbiol. 1:259-273(1987).
 RN [6]
 RX IDENTIFICATION.
 RX MEDLINE=96032851; Pubmed=7567469;
 RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
 RA Danchin A.;
 RT "Detection of new genes in a bacterial genome using Markov models for
 RT three gene classes.";
 RL Nucleic Acids Res. 23:3554-3562(1995).
 CC -1- SIMILARITY: TO E.COLI YDEK.
 CC -1- CAUTION: Ref.3 sequence differs extensively from that shown by
 CC many frameshifts.
 CC -----
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 CC -----
 DR EMBL; AB000313; AAC75293.1; -
 DR EMBL; D90855; BAA16052.1; ALT INIT.
 DR EMBL; D90854; BAA16050.1; ALT INIT.
 DR EMBL; K02672; -; NOT ANNOTATED_CDS.
 DR EMBL; U30459; AAA74094.1;
 DR EMBL; Y00544; -; NOT ANNOTATED_CDS.
 DR PIR; G64993; G64993.
 DR Ecogene; EG12850; yfal.
 DR InterPro; IPR006315; Autoctransport.
 DR InterPro; IPR005546; Autoctransport.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR InterPro; IPR004899; Pertactin.
 DR Pfam; PF03797; Autoctransport; 1.
 DR Pfam; PF02415; Chlamydia_PMP; 1.
 DR Pfam; PF03212; Pertactin; 1.
 DR TIGRFAMs; TIGR01414; autoctrans bar1; 2.
 DR TIGRFAMs; TIGR01376; POMP repeat; 4.
 DR Hypothetical protein; Repeat; Signal; Complete proteome.
 KM
 FT SIGNAL 1 23
 FT CHAIN 24 1250
 FT DOMAIN 919 948
 FT FT 28 30
 FT CONFLICT 40 40
 FT CONFLICT 65 66
 FT CONFLICT 431 431
 FT CONFLICT 433 433
 FT CONFLICT 478 478
 FT CONFLICT 773 773
 FT CONFLICT 853 853
 FT CONFLICT 923 924
 FT CONFLICT 948 994
 SQ SEQUENCE 1250 AA; 131152 MW; 17980505299C95 CRC64;
 Query Match 6.6%; Score 113.5; DB 1; Length 1250;
 Best Local Similarity 21.9%; Pred. No. 18;
 Matches 90; Conservative 45; Mismatches 137; Indels 139; Gaps 19;
 QY 4 ADAPAGDTINQLTN---VTVGIDS-----GTVVPHQAGVYK----- 40
 DB 618 SDAAGHGDIMRADGEVAVDAGVDTQMGALMADSSGQHODBSGTLTKTGAAGTLELASG 677
 QY 41 --NYGFSVNSAVKGFITKIVPELNL---NGVTSTAKVPPIWAGQVLANGVID-SDG 94
 DB 678 TTQSAVRVEESGTLKGVADI-LPYASSLWWDGATFTGTGADODIOSIDAISGTTIDISDG 736
 QY 95 NVI-YTFRD-----YVNTKDVAKTLMPAYIDP-----NYKKTGNVT 132
 DB 737 TVLRITGDTVALNALSFNQDGLVNAATDGVTLTGLNTRLEFDSLTSYNTVANGNLT 796
 QY 133 LATGI-----GSTTANKTVLVDEKYKGFNLSIKGTIDQDKTNNYRQ 177

```

Db 797 NTSGAVSLQNGVADLTLTNGDYTGCGTLLDLSLNGD-----DSVSDQVNMNGTAGN 850
Qy 178 TIYVPSGDNVIAPELTGNLKPNFTDSNALIDQNTSIKRYKVDNAD-----LS 226
Db 851 T-----TIVVNSITGIGEP-----STGIKV--VDFADPTQFQNNAPSLA 890
Qy 227 ESYFVN-----PENFEDVTSVNT-----FPNPNQYKVEFNPDDQITTPY 268
Db 891 GSGYVNGKAYITLTVEDNNWYTLASQEVTPPSPPDPPTPDPTPDPTPDPTPDPT 950
Qy 269 IVVYNGHIDPNSKGLALRSTLYGNSNIWRMSWDNEVAFNNGSGSDG 319
Db 951 QPVNAKVG-----GYLNILRAANQAFWME---RDHAGDGD 984

RESULT 14
PIP LACLC STANDARD; PRT; 1902 AA.
AC P16271;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P1-type proteinase precursor (EC 3.4.21.-) (Wall-associated serine
  proteinase).
GN PRTP.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG2;
RX MEDLINE=88149035; PubMed=3278687;
RA Kok J., Leenhouts K.J., Haandrikman A.J., Ledeboer A.M., Venema G.;
  "Nucleotide sequence of the cell wall proteinase gene of
  Streptococcus cremoris MG2.";
  J. Biol. Chem. 268:231-238(1993).
RT Appl. Environ. Microbiol. 54:231-238(1998).
RL
CC -1- FUNCTION OF THE BACTERIA WHICH BREAKS DOWN MILK PROTEINS DURING THE
  GROWTH OF THE BACTERIA ON MILK.
CC -1- CATALYTIC ACTIVITY: Endopeptidase activity with very broad
  specificity, although some substrate preference have been noted,
  e.g. large hydrophobic residues in the P1 and P4 positions, and
  Pro in the P2 position. Best known for its action on caseins,
  although it has been shown to hydrolyze hemoglobin and oxidized
  insulin B-chain.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
  an amide bond (Potential).
CC -1- SIMILARITY: Belongs to peptidase family S8.
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CC
DR EMBL: M24767; AAA17677.1; -
DR HSSP: P00782; 1S01.
DR MEROPS: S08.019; -
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR003137; PA.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam: PF00746; Gram_pos_anchor_1.
DR Pfam: PF02325; PA_1.
DR Pfam: PF00682; Peptidase_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR TIGRPFAM: TIGR01167; LFXG_anchor_1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.

```

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KM Hydrolase; Serine protease; Cell wall; peptidoglycan-anchor; Zymogen;
KW Signal; Plasmid.
FT SIGNAL 1 33
FT PROPEP 34 187
FT CHAIN 188 1870
FT PROPEP 1871 1902
FT ACT SITE 217 217
FT ACT SITE 281 281
FT ACT SITE 620 620
FT SITE 1867 1871
FT MOD_RES 1870 1870
SQ SEQUENCE 1902 AA; 199910 MW; 2901C7F19B2E5D0B CRC64;

Query Match 6.6%; Score 113.5; DB 1; Length 1902;
Best Local Similarity 21.1%; Pred. No. 30;
Matches 71; Conservative 35; Mismatches 100; Indels 131; Gaps 14;

Qy 3 AADAPAGTDITNQ-----LTNVTGIDSGT-----TYYPHAGYVKL- 40
Db 506 AQAGAGAGLIVNNGTATPVTSMALLTTPPTFGLSVTGQKLVWVTAHPDLSGVKIA 565
Qy 41 -----NYGFSVPNSAVKAGDTFKIYV-----XELNIGVTS---TAK 74
Db 566 LTLVPNQKTEDKMSDFTSYG--PVSNLSFKPD---ITAPGNIWSTQNNNGYTNNSGTSM 621
Qy 75 VPPIMAGDQVLANGVDSQGNVITF-----TDYNTKDDYKATLTMPAYIDPENV 125
Db 622 ASPFIAGSQALKQALNNKNNPFAVYKQKGTALDFEKT-----VENNTA 668
Qy 126 KKTGNVTLATGISSTANKTVLVDEYKGFYNLISIKGTIDQIDK----- 170
Db 669 QPINDINNVNVIYSPRQAGALVD-----YKAIDALEKNPSTVAENGYPAYE 717
Qy 171 -----TNNTYROTIVNPSGDNVIAPELTGNLKPNFTDSNAL-----IDQNTSIKRYKVD 220
Db 718 LKDFSTDKFKLTF-----TWSTTHELTLYQMSVTDNNAVYATSDPNSGLVDKDKID 771
Qy 221 NAADLESYFVNPNEDVTSVNTFPNPNQYKVEF 257
Db 772 GAA-----IKAGSNITVPAGKTAQIEF 793

RESULT 15
P2P LACPA
ID P2P LACPA STANDARD; PRT; 1902 AA.
AC Q02470;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P1-type proteinase precursor (EC 3.4.21.96) (Lactocoeplin) (Cell wall-
  associated serine proteinase) (Lp151).
GN GN
OS Lactobacillus paracasei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
  Lactobacillus.
OC NCBI_TaxID=1597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCDO 151;
RX MEDLINE=92381481; PubMed=1512565;
RA Holck A., Naes H.;
  "Cloning, sequencing and expression of the gene encoding the cell-
  envelope-associated proteinase from Lactobacillus paracasei subsp.
  RT paracasei NCDO 151.";
  J. Gen. Microbiol. 138:1353-1364(1992).
RL
RN [2]
RP SEQUENCE OF 189-196.
RX MEDLINE=92226694; PubMed=1564442;
RA Naes H., Nissen-Meyer U.;
  "Purification and N-terminal amino acid sequence determination of the
  cell-wall-bound proteinase from Lactobacillus paracasei subsp.
  RT paracasei.";
  J. Gen. Microbiol. 138:313-318(1992).

```

CC - FUNCTION: PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE
 CC GROWTH OF THE BACTERIA ON MILK.
 CC - CATALYTIC ACTIVITY: Endopeptidase activity with very broad
 CC specificity, although some substrate preference have been noted,
 CC e.g. large hydrophobic residues in the P1 and P4 positions, and
 CC pro in the P2 position. Best known for its action on caseins,
 CC although it has been shown to hydrolyze hemoglobin and oxidized
 CC insulin B-chain.
 CC - SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC - SIMILARITY: Belongs to peptidase family S8.
 CC
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 CC
 CC EMBL; M83946; AAA25248.1; -
 CC PIR; B44858; B44858.
 CC HSSP; P00782; I501.
 CC MEROPS; S08.019; -
 CC InterPro; IPR001899; Gram_pos_anchor.
 CC InterPro; IPR003137; PA.
 CC InterPro; IPR000209; Peptidase_S8.
 CC Pfam; PF00746; Gram_pos_anchor; 1.
 CC Pfam; PF02225; PA; 1.
 CC Pfam; PF00082; Peptidase_S8; 1.
 CC PRINTS; PR00723; SUBTILISIN.
 CC TIGRPFMS; TIGR01167; LPTG_anchor; 1.
 CC PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.
 CC PROSITE; PSS00136; SUBTILASE_ASP; 1.
 CC PROSITE; PSS00137; SUBTILASE_HIS; 1.
 CC PROSITE; PSS00138; SUBTILASE_SER; 1.
 CC K1M Hydrolyase; Serine protease; Cell wall; Peptidoglycan-anchor; Zymogen;
 CC Signal.
 CC FT SIGNAL 1 33
 CC FT PROPEP 34 187
 CC FT CHAIN 188 1870
 CC PROPEP 1871 1902
 CC ACT_SITE 217 217
 CC ACT_SITE 281 281
 CC ACT_SITE 620 620
 CC SITE 1867 1871
 CC MOD RES 1870 1870
 CC SEQUENCE 1902 AA; 200253 MW; D8C9F38CE5DA582 CRC64;
 SQ
 Query Match 6.6%; Score 113.5; DB 1; Length 1902;
 Best Local Similarity 23.2%; Pred. No. 30;
 Matches 76; Conservative 35; Mismatches 104; Indels 113; Gaps 17;
 QY 3 AADPAAGTITNQ-----LTNV-----TVGIDSGT-----TVYRQAGYKL- 40
 Db 506 AQAAGAGLITVNDGATPPTLSIRLTPTTPTFGLSKTGCKLVDTAHPDSDLGKTA 565
 QY 41 -----NYGFSVNSAVKGDTPFKITVP-----KEINLVGVS--TAK 74
 Db 566 LTLPNKYTEDKMSDFTSYG-PVSNLSFKPD--ITAPGNIMSTQNNNGYTMMSGTSM 621
 QY 75 VPEPMAGDOVLANGVDSGNVITFTDYNTKDVAKILMPAYIDPEVKKTGNTLA 134
 Db 622 ASPPIASQALLKQALNNKNPFY--ADYKQLKG--TALT-----DFLKTIVEMNTA 668
 QY 135 TGIGSTTANKTVLVDEYKGFYNLSIKGIDQIDK-----TNN 173
 Db 669 QPINDINN-NVIVSPRQAGL--VDYKAIDALEKPSVVAENGYPAVELKDFSTDK 726
 QY 174 TYRQTIYVNSGDVIAVLGNLKPNYDSNAL-----IDQNTSIRKYKYVDNADLSESY 229
 Db 727 TFKLTF-----TNRTHELTYQMSDNTDINAAYVTSATDPNSGVLVDKRIDGAA----- 774

QY 230 FVNPEVEDVTSVNTTFPENQYKVEF 257
 Db 775 -----IKAGSDITVPAGKTAOLEF 793
 Search completed: March 26, 2004, 05:04:45
 Job time : 25.9539 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 05:07:57 ; Search time 1044.06 Seconds

(without alignments)
82.955 Million cell updates/sec

Title: US-10-056-052a-4

Perfect score: 1732
Sequence: 1 WVAADAPAGTDITNQLTNV.....NGSGSGDGIDKPVPEQPD 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 segs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

Result No.	Score	Query Length	DB ID	Description
1	1732	100.0	331	US-10-056-052-4
2	1732	100.0	345	US-09-813-820-7
3	1727	99.7	520	US-10-056-052-2
4	1723	99.5	936	US-08-781-986A-5249
5	1723	99.5	936	US-10-329-624-5249
6	1518	87.6	1021	US-09-815-242-5471
7	1518	87.6	1021	US-09-815-242-12544
8	1517	87.6	935	US-10-282-122A-44326
9	1433	82.7	496	US-10-311-879-29
10	416.5	24.0	961	US-10-282-122A-43778
11	409	23.6	767	US-09-815-242-5899
12	409	23.6	767	US-09-815-242-13140
13	353	20.4	343	US-10-378-674-4
14	353	20.4	560	US-10-378-674-2
15	353	20.4	892	US-10-282-122A-70481

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	353	20.4	930	12	US-10-615-383-10	Sequence 10, Appli
17	349	20.2	549	15	US-10-378-674-9	Sequence 9, Appli
18	349	20.2	1092	15	US-10-378-674-8	Sequence 8, Appli
19	346	20.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
20	346	20.0	1001	9	US-09-815-242-13686	Sequence 12686, A
21	338	19.6	1018	9	US-09-815-242-5797	Sequence 5797, Ap
22	339	19.6	1018	9	US-09-815-242-12838	Sequence 12838, A
23	331	19.1	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
24	331	19.1	1027	12	US-10-329-624-5254	Sequence 43827, A
25	324.5	18.7	1038	12	US-10-282-122A-43827	Sequence 43827, A
26	320.5	18.5	1141	12	US-10-282-122A-70251	Sequence 70251, A
27	312.5	18.0	877	12	US-10-282-122A-70428	Sequence 70428, A
28	304.5	17.6	316	15	US-10-378-674-6	Sequence 6, Appli
29	282.5	16.3	251	8	US-08-781-986A-5252	Sequence 5252, Ap
30	282.5	16.3	251	12	US-10-329-624-5252	Sequence 5896, Ap
31	257.5	14.9	1349	9	US-09-815-242-5898	Sequence 13137, A
32	257.5	14.9	1349	9	US-09-815-242-13137	Sequence 44324, A
33	240.5	13.9	1385	12	US-10-282-122A-44324	Sequence 5578, Ap
34	232.5	13.4	932	9	US-09-815-242-5578	Sequence 12438, A
35	232.5	13.4	932	9	US-09-815-242-12438	Sequence 44457, A
36	229.5	13.3	953	12	US-10-282-122A-44457	Sequence 71413, A
37	212.5	12.3	1920	12	US-10-282-122A-71413	Sequence 5779, Ap
38	210.5	12.2	841	9	US-09-815-242-5779	Sequence 12751, A
39	210.5	12.2	841	9	US-09-815-242-12751	Sequence 70437, A
40	201.5	11.6	1633	12	US-10-615-383-4	Sequence 70444, A
41	201.5	11.6	1742	12	US-10-282-122A-70444	Sequence 2, Appli
42	187.5	10.8	670	12	US-10-381-556A-2	Sequence 57884, A
43	140	8.1	2060	15	US-10-282-122A-57384	Sequence 46817, A
44	139.5	8.1	628	12	US-10-282-122A-46817	
45	139	8.0	3930	12	US-10-282-122A-46817	

ALIGNMENTS

RESULT 1
US-10-056-052-4
Sequence 4, Application US/10056052
Publication No. US20030099656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
FILE REFERENCE: P0706904/BAS
CURRENT APPLICATION NUMBER: US/10/056, 052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 331
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-4

Query Match 100.0%; Score 1732; DB 14; length 331;
Best Local Similarity 100.0%; Pred. No. 9, 6e-139;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVAADAPAGTDITNQLTNVTVGGTITVPHQAGVYKNGFSVNSAVKDGTFITV 60
DB 1 WVAADAPAGTDITNQLTNVTVGGTITVPHQAGVYKNGFSVNSAVKDGTFITV 60

QY 61 PKEINLVSTAKVPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLMPAYI 120
DB 61 PKEINLVSTAKVPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLMPAYI 120
QY 121 DENVAKTGNVTLATIGSTTANKTVLVDEYKGFYNSIKGTLIDQIDKTNNTYRQITLY 180
DB 121 DENVAKTGNVTLATIGSTTANKTVLVDEYKGFYNSIKGTLIDQIDKTNNTYRQITLY 180
QY 181 VNPSCGNVIAPVLTGMLKNTDSNALIDQNTSIKYYKVDNAADLSESYFVNPFEDVT 240
DB 181 VNPSCGNVIAPVLTGMLKNTDSNALIDQNTSIKYYKVDNAADLSESYFVNPFEDVT 240
QY 241 NSVNTFPNPNQYKVEFNTDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMR 300
DB 241 NSVNTFPNPNQYKVEFNTDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMR 300
QY 301 SMSWNEVAFNNGSGSGDIDKPVPEQDPE 331
DB 301 SMSWNEVAFNNGSGSGDIDKPVPEQDPE 331

RESULT 2
US-09-813-820-7
Sequence 7, Application US/09813820
Patent No. US20020102262A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

Pattl, Joseph M.

House-Pompeo, Karen

Shanahan, Nataraya

Symesky, Jindrich

TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS

AND METHODS OF USE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: U.S.

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/813, 820

FILING DATE: 22-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/856,253

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: TAWK.193

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 345 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-813-820-7
Query Match 100.0%; Score 1732; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 1e-138;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAADAPAGTIDITNOLTNVTVGIDSGTTPYHPQAGYVKNLNGFSVPNSAVKDGTFKITV 60
DB 13 MVAADAPAGTIDITNOLTNVTVGIDSGTTPYHPQAGYVKNLNGFSVPNSAVKDGTFKITV 72
QY 61 PKEINLVSTAKVPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLMPAYI 120
DB 73 PKEINLVSTAKVPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLMPAYI 132
QY 121 DENVAKTGNVTLATIGSTTANKTVLVDEYKGFYNSIKGTLIDQIDKTNNTYRQITLY 180
DB 133 DENVAKTGNVTLATIGSTTANKTVLVDEYKGFYNSIKGTLIDQIDKTNNTYRQITLY 192
QY 181 VNPSCGNVIAPVLTGMLKNTDSNALIDQNTSIKYYKVDNAADLSESYFVNPFEDVT 240
DB 193 VNPSCGNVIAPVLTGMLKNTDSNALIDQNTSIKYYKVDNAADLSESYFVNPFEDVT 252
QY 241 NSVNTFPNPNQYKVEFNTDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMR 300
DB 253 NSVNTFPNPNQYKVEFNTDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMR 312
QY 301 SMSWNEVAFNNGSGSGDIDKPVPEQDPE 331
DB 313 SMSWNEVAFNNGSGSGDIDKPVPEQDPE 343

RESULT 3

US-10-056-052-2

Sequence 2, Application US/10056052

Publication No. US20030099656A1

GENERAL INFORMATION:

APPLICANT: PATTL, Joseph M

APPLICANT: HUTCHINS, Jeff T

APPLICANT: DOMANSKI, Paul

APPLICANT: PATEL, Pratiksha

APPLICANT: HALL, Andrea

TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

FILE REFERENCE: P07069US04/BAS

CURRENT APPLICATION NUMBER: US/10/056,052

PRIOR APPLICATION NUMBER: 60/308,116

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/298,413

PRIOR FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: 60/274,611

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: 60/264,072

PRIOR FILING DATE: 2001-01-26

SOFTWARE: Patentin version 3.1

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 2

LENGTH: 520

TYPE: prt

ORGANISM: Staphylococcus aureus

US-10-056-052-2
Query Match 99.7%; Score 1727; DB 14; Length 520;
Best Local Similarity 100.0%; Pred. No. 5e-138;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAAADAPAGTIDITNOLTNVTVGIDSGTTPYHPQAGYVKNLNGFSVPNSAVKDGTFKITV 61
DB 183 VAAADAPAGTIDITNOLTNVTVGIDSGTTPYHPQAGYVKNLNGFSVPNSAVKDGTFKITV 241
QY 62 KKLINLVSTAKVPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLMPAYI 121
DB 243 KKLINLVSTAKVPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLMPAYI 301
QY 122 DENVAKTGNVTLATIGSTTANKTVLVDEYKGFYNSIKGTLIDQIDKTNNTYRQITLY 181
DB 302 DENVAKTGNVTLATIGSTTANKTVLVDEYKGFYNSIKGTLIDQIDKTNNTYRQITLY 361
QY 182 NSGDNVIAPVLTGMLKNTDSNALIDQNTSIKYYKVDNAADLSESYFVNPFEDVTN 241

Db 362 NPSGDNVIAPLYLTGNLKENTDSNALIDQONTSIKVKYVDNADLSESYFVNPFEDVTN 421
Qy 242 SVNITFPNPQYKVEFNPDPDOITTPYIVVNGHIDPNSKGDALRSTLYGNSNIWRS 301
Db 422 SVNITFPNPQYKVEFNPDPDOITTPYIVVNGHIDPNSKGDALRSTLYGNSNIWRS 481
Qy 302 MSWDNEVAFNNNGSGSDGIDKPVPEQDPE 331
Db 482 MSWDNEVAFNNNGSGSDGIDKPVPEQDPE 511

RESULT 4

US-08-781-986A-5249
Sequence 5249, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5235
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5249:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5249

Query Match 99.5%; Score 1723; DB 8; Length 936;
Best Local Similarity 99.7%; Pred. No. 2,6e-137;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 VAADAPAGTDTITNLTNTVVGIDSGTTPYPHOAGYKLVGSPVNSAVKGDITFKITVP 61
Db 230 VAADAPAGTDTITNLTNTVVGIDSGTTPYPHOAGYKLVGSPVNSAVKGDITFKITVP 289
Qy 62 KEINLVGVTSTAKVPIMAGDQVLANGVIDSDGNVIYTFDYNTKDVKATLTMPAYID 121
Db 290 KEINLVGVTSTAKVPIMAGDQVLANGVIDSDGNVIYTFDYNTKDVKATLTMPAYID 349
Qy 122 PENVKKTGVNLTATGIGSTTANKTVLVDEKYGKFNLSIKGIIIDIKTNNTYQGITIV 181
Db 350 PENVKKTGVNLTATGIGSTTANKTVLVDEKYGKFNLSIKGIIIDIKTNNTYQGITIV 409
Qy 182 NPSGDNVIAPLYLTGNLKENTDSNALIDQONTSIKVKYVDNADLSESYFVNPFEDVTN 241
Db 410 NPSGDNVIAPLYLTGNLKENTDSNALIDQONTSIKVKYVDNADLSESYFVNPFEDVTN 469

Qy 242 SVNITFPNPQYKVEFNPDPDOITTPYIVVNGHIDPNSKGDALRSTLYGNSNIWRS 301
Db 470 SVNITFPNPQYKVEFNPDPDOITTPYIVVNGHIDPNSKGDALRSTLYGNSNIWRS 529
Qy 302 MSWDNEVAFNNNGSGSDGIDKPVPEQDPE 331
Db 530 MSWDNEVAFNNNGSGSDGIDKPVPEQDPE 559

RESULT 5

US-10-329-624-5249
Sequence 5249, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5249:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5249:
US-10-329-624-5249

Query Match 99.5%; Score 1723; DB 12; Length 936;
Best Local Similarity 99.7%; Pred. No. 2,6e-137;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 VAADAPAGTDTITNLTNTVVGIDSGTTPYPHOAGYKLVGSPVNSAVKGDITFKITVP 61
Db 230 VAADAPAGTDTITNLTNTVVGIDSGTTPYPHOAGYKLVGSPVNSAVKGDITFKITVP 289
Qy 62 KEINLVGVTSTAKVPIMAGDQVLANGVIDSDGNVIYTFDYNTKDVKATLTMPAYID 121
Db 290 KEINLVGVTSTAKVPIMAGDQVLANGVIDSDGNVIYTFDYNTKDVKATLTMPAYID 349

QY	122	PEUVKKTGAVTLATGIGSGTAKTATLVYKKGKRYNLSIGTLDQIDKNNYRQITIV	181
Db	350	PEUVKKTGAVTLATGIGSGTAKTATLVYKKGKRYNLSIGTLDQIDKNNYRQITIV	409
QY	182	NPESGDVIAPIVLTGNLKPNTDSNALIDQNTSISKVYKVDNADISESYFVNPFEDVTN	241
Db	410	NPESGDVIAPIVLTGNLKPNTDSNALIDQNTSISKVYKVDNADISESYFVNPFEDVTN	469
QY	242	SVNITFPENQYKVENVTDPDDQITTPYLYVNGHIDPMSKQDLRLSTLYGNSNIITWS	301
Db	470	SVNITFPENQYKVENVTDPDDQITTPYLYVNGHIDPMSKQDLRLSTLYGNSNIITWS	529
QY	302	MSMDNEVAFNNGSGSGDGIDKPIVPEQDPE	331
Db	530	MSMDNEVAFNNGSGSGDGIDKPIVPEQDPE	559

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RESULT 6
US-09-815-242-5471
; Sequence 5471, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haeselbeck, Robert
APPLICANT: Onlssen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/121,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,525
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5471
LENGTH: 1021
TYPE: FRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5471

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Query Match	Similarity	87.6%	Score 1518	DB 9	Length 1021
Best Local	Similarity	87.3%	Pred. No. 7.6e-120		
Matches	288	Conservative	17	Mismatches	25; Indels 0; Gaps 0
QY	2	VAADAPAACTDITNQTNTTVGIDSGTYYPHQAGYVKLNKGFVSNSAVKXGDTFTIYV	61		
DB	221	VAADAPAACTDITNQTNTTVGKTLIDSGTYYPHQAGYVKLNKGFVSNSAVKXGDTFTIYV	280		
QY	62	KEILNLTGVTSTAKVPPIMAGDOVLANGVTDSDGNVYTTTDTYNTKDDVKAULTMPAYID	121		
DB	281	KEILNLTGVTSTAKVPPIMAGDOVLANGVTDSDGNVYTTTDTYNTKDDVKAULTMPAYID	340		
QY	122	PENVKKTGAVTLATGISTTAKTIVVDYEEKGFNLISIKGTLIDIDIKNTNTRYOTIYV	181		
DB	341	PENVKKTGAVTLATGISTTAKTIVVDYEEKGFNLISIKGTLIDIDIKNTNTRYOTIYV	400		

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QY 182 NBSGDNVIA.PVLTGLKPTNSNALIDQUNSIKYKVDNAADSESYFANPEFEEVYN 241
Db 401 NBSGDNVVVPALTGLILPWTKSNNALIDAKNDIKYKVDNANDISESYYNPSDFELVYN 460
QY 242 SVNITFEPNENQKVEFENFTPDQITTPYLVVNGHIDPNKGDLLRSTLYGYSNNIIMRS 301
Db 461 QVRIISFPNANQKVEFEPIDDDQITTPYLVVNGHIDPASTDILLRSTFYGYDSNFIIMRS 520
QY 302 MSWNDNEVAFNNGSGSDGIDKPVVEQDPE 331
Db 521 MSWNDNEVAFNNGSGSDGIDKPVVEQDDE 550
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US-09-815-242-12544
RESULT 7
; Sequence 12544, Application US/09815242
; Patent No. US2002061869A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12544
; LENGTH: 1021
; TYPE: prf
; ORGANISM: Staphylococcus aureus
US-09-815-242-12544

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Query Match	87.6%	Score 1518;	Length 1021;
Best Local Similarity	87.3%	Pred. No. 7,6e+120;	
Matches	288;	Conservative 17;	Mismatches 25; Indels 0; Gaps 0;

QY	2	VAADPAAGTDITNOLINVTYGI	DSGTTVY	PHOAGYKLAN	GESVPNSAVNGDFFIKV	61	
		21	VAADPAAGTDITNOLINVTYK	ITDSGTTVY	PHOAGYKLAN	GESVPNSAVNGDFFIKV	280
QY	62	KELINAGVTSTAKVPPIMAGQ	VLANGV	ISDGNVIYFT	FDYVNTK	ODVKATLIMPAYID	121
DB	281	KELINAGVTSTAKVPPIMAGQ	VLANGV	ISDGNVIYFT	FDYVNTK	ODVKATLIMPAYID	340
QY	122	PENVTAKGTGNVLATISG	STANKTVLV	YEKKGYNT	SISGTDID	QIDKTNNTYRQITVY	181
DB	341	PENVTAKGTGNVLATISG	STANKTVLV	YEKKGYNT	SISGTDID	QIDKTNNTYRQITVY	400
QY	182	NSGSGNVIAFVLTKMLK	ENPTSNAL	IDQNTS	SIKKYK	DNAADISESYFVNPNEDVTN	241
DB	401	NSGSGNVIAFVLTKMLK	ENPTSNAL	IDAKNTD	IKYRV	DNANDISESYFVNPNEDVTN	460

QY 242 SVNTTFPNNQYKVEFNTDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 461 QVRISFPNANQYKVEFNTDDQITTPYIVVNGHIDPASTGDLALRSTLYGNSNIIMRS 520
QY 302 MSWDNEVAFNNNGSGSDGIDKPVPEQPDE 331
DB 521 MSWDNEVAFNNNGSGSDGIDKPVPEQPDE 550

RESULT 8
US-10-282-122A-44326
Sequence 44326, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA 0344
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44326
LENGTH: 935
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-10-282-122A-44326

Query Match 87.6%; Score 1517; DB 12; Length 935;
Best Local Similarity 87.3%; Pred. No. 8,1e-120;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 VAADAPAGDITNTQNLNVVIGDSGTTVPHQAGYKLVNNGSVNSAVKGTFTKTV 61
DB 221 VAADAPAGDITNTQNLNVVIGDSGTTVPHQAGYKLVNNGSVNSAVKGTFTKTV 280
QY 62 KELNNGVSTAKVPPIAGDQVLANGVIDSDGNVITFTDYNTKODVAKTLTMPAYID 121
DB 281 KELNNGVSTAKVPPIAGDQVLANGVIDSDGNVITFTDYNTKODVAKTLTMPAYID 340
QY 122 PENYKGTGNVTLAIGISTTANKTVLVDEYKYGKFNLSIKGTIDQDKNTNTRQTIYV 181

DB 341 PENYKGTGNVTLAIGISTTANKTVLVDEYKYGKFNLSIKGTIDQDKNTNTRQTIYV 400
QY 182 NPSGDNVIAVLTGNLKPNTDSNALIDQNTSIRKYKYDNADLESYFVNPEFEDVTN 241
DB 401 NPSGDNVIAVLTGNLKPNTDSNALIDQNTSIRKYKYDNADLESYFVNPEFEDVTN 460
QY 242 SVNTTFPNNQYKVEFNTDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 461 QVRISFPNANQYKVEFNTDDQITTPYIVVNGHIDPASTGDLALRSTLYGNSNIIMRS 520
QY 302 MSWDNEVAFNNNGSGSDGIDKPVPEQPDE 331
DB 521 MSWDNEVAFNNNGSGSDGIDKPVPEQPDE 550

RESULT 9
US-10-311-879-29
Sequence 29, Application US/10311879
Publication No. US20030186275A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
TITLE OF INVENTION: Antigenic Peptides
FILE REFERENCE: tox1n
CURRENT APPLICATION NUMBER: US/10/311,879
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 496
TYPE: PRF
ORGANISM: Staphylococcus aureus
US-10-311-879-29

Query Match 82.7%; Score 1433; DB 14; Length 496;
Best Local Similarity 100.0%; Pred. No. 4,3e-113;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGDITNTQNLNVVIGDSGTTVPHQAGYKLVNNGSVNSAVKGTFTKTV 61
DB 221 VAADAPAGDITNTQNLNVVIGDSGTTVPHQAGYKLVNNGSVNSAVKGTFTKTV 280
QY 62 KELNNGVSTAKVPPIAGDQVLANGVIDSDGNVITFTDYNTKODVAKTLTMPAYID 121
DB 281 KELNNGVSTAKVPPIAGDQVLANGVIDSDGNVITFTDYNTKODVAKTLTMPAYID 340
QY 122 PENYKGTGNVTLAIGISTTANKTVLVDEYKYGKFNLSIKGTIDQDKNTNTRQTIYV 181
DB 341 PENYKGTGNVTLAIGISTTANKTVLVDEYKYGKFNLSIKGTIDQDKNTNTRQTIYV 400
QY 182 NPSGDNVIAVLTGNLKPNTDSNALIDQNTSIRKYKYDNADLESYFVNPEFEDVTN 241
DB 401 NPSGDNVIAVLTGNLKPNTDSNALIDQNTSIRKYKYDNADLESYFVNPEFEDVTN 460
QY 242 SVNTTFPNNQYKVEFNTDDQITTPYIVVNGHID 277
DB 461 SVNTTFPNNQYKVEFNTDDQITTPYIVVNGHID 496

RESULT 10
US-10-282-122A-43778
Sequence 43778, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant

```

APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43778
LENGTH: 961
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

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Query Match      24.0%; Score 416.5; DB 12; Length 961;
Best Local Similarity 29.1%; Pred. No. 2,5e-26;
Matches 101; Conservative 69; Mismatches 144; Indels 33; Gaps 9;

QY 2 VAADAPAGDTITNLTNTVTVGID---SGTTPYHQAQGVKLYNGSPVNSAVKDDTK 57
DB 158 VAEAKATGTDVINKVETVSSLEGHNKDSNIVNPHNAQCVTLKYMKGEGIKADYD 217
QY 58 ITVEKELNGLVSTAVPPIIMAG--DQVLANGVIDSGNVITFPDYVNTKDVATLT 115
DB 218 FTLSDNVETHTGISLTRVPEIKSTEDKVNAGQVINERTIRITFDYINNKDULAEIN 277
QY 116 MPAYIDPENYKGTGNVTLATIGSTTANKTVLVY---EKYGEFYNLSIKGTIDQIDK 170
DB 278 LNFIDIDPTVTKQSQKVEVTLTGONKYSKEFDIKYLDGVKDRMG---VTNNGRIDTLNK 333
QY 171 TNNYRQTIYVNSGDNVIAVLTGNLKPTDGNALIDQNTSIRKYKVDNADLSSEYF 230
DB 334 EEEKFSFAAYKPPNQSILSTVYTGQVTSYGKOSA---NNPVTKYKHIGSELLESYV 389
QY 231 V---NPNFEDVTSVNITFPNPNQYKVEFNTPPDQITTPYIVVNGHIDPNSKGLALR 287
DB 390 AKLDDTSKFEVETKVLSTNSNGYTLNLGDLDN--SKDYVIKYEGEYDQNAK-DLNR 446
QY 288 STLYGYSNITWR-----SMGNDVAFNNGSGGDDIDFVVP 326
DB 447 THLSGKHXYYPYYPYVQVLTWNNGVAFYSSNNAKGDKDKENDP 493

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RESULT 11
US-09-815-242-5899
Sequence 5899, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zykkind, Judith W.

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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5899
LENGTH: 767
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5899

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Query Match      23.6%; Score 409; DB 9; Length 767;
Best Local Similarity 28.9%; Pred. No. 7.7e-26;
Matches 101; Conservative 72; Mismatches 131; Indels 46; Gaps 11;

QY 2 VAADAPAGDTITNLTNTVTVGIDSGT-----TVYHQAQGVKLYNGSPVNSAV 51
DB 155 VVEBKATGTDVINK-----VEVEGESEIVGHKQDTVNVNPHNAQCVTLKYMKGEGIK 209
QY 52 KQDTPKTIPEKELNGLVSTAKVPPIIMAGD-QVLANGVIDSGNVITFPDYVNTKDDV 110
DB 210 AGDYFDFLSDNVETHGISTLRKVPKIKSTDGQVMAQGEIIGEKVYTFREIYQEKDL 269
QY 111 KATLMPAYIDPENYKGTGNVTLATIGSTTANKTVLVY---EKYGEFYNLSIKGTI 165
DB 270 TAEISLNFIDPTVTKQSGNVNVEKLGETTYSKIFNIQYLGVRDNMG---VTANGRI 325
QY 166 DQIDKXNTYRQTIYVNSGDNVIAVLTGNL---KPTDGNALIDQNTSIRKYKVDN 221
DB 326 DTLNKVDKFSHFVPMKPNQSLSSVTVTGQVTKGNRQVNA-----NPTVRYVHIG 377
QY 222 AADLSSEYFVNPN---FEDVTSVNITFPNPNQYKVEFNTPPDQITTPYIVVNGHIDP 278
DB 378 SDDLAESVYAKLDVSKEDVTDMNSLDFDTNGYSILNFINLDQ--SKNYIKYEGYDS 435
QY 279 NSKGLALRSTLYGYSNIIWRSMWDEVAFNNGSGGDDIDK---PVV 325
DB 436 NAFSLERQTHLFGYNYNYTSNLTWNKGVAFYSSNNAKGDKDKXIKPEII 484

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RESULT 12
US-09-815-242-13140
Sequence 13140, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.

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; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13140
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13140

Query Match          23.6%; Score 409; DB 9; Length 767;
Best Local Similarity 28.9%; Pred. No. 7.7e-26;
Matches 101; Conservative 72; Mismatches 131; Indels 46; Gaps 11;

QY 2 VAADAAAGTDTTNTLTNTVVGIDSGT-----TYPHOAGYVKLNGFSPVNSAV 51
DB 155 VVEETKATGTDVTK-----VEVEBSSEIVGHKODTNVNPVNAEVTLKRYMKKEGEGIK 209
QY 52 KGDPTKIVPEKLNGLVSTAKVPIMAGD-OVLANGYDSDGNITYFTFYVNTKDDV 110
DB 210 AGYFPFTLSDNVETHGISLTKRVPBKSTDSQVMAIGELIGRKRYTFKRYVEGCKDL 269
QY 111 KATLTPPAYIDPENKKTGNVTLATIGSTTANKTVLVY---EKYKFPNLSIKGTI 165
DB 270 TAEIISNLFIIDPTTVYQKGNQNEVKLGGETVSKIFNIQYLGGVRDNMG---VTANGRI 325
QY 166 DQDXTNNTKQRTIYVNPSSGVNIAPVLGNL-----KPTMSNALIDQNTSIKYKXVDN 221
DB 326 DTLNKVDGKSHRAVYKKNQSSLSVTVIGQVTKKPKGVN-----NPTVYKIKHIG 377
QY 222 AADLSSYFVNPN--FEDVINSVNIITPENPNQYKVEFTPDQITTFYIVVNGHIDP 278
DB 378 SDDLASSVYAKLDVSGFEFEDVTDMSLDFTNGYSILNPNLDQ--SKNYVIKRYEGYDS 435
QY 279 NSGGLALRSTLIGYNSNIWRSMWMDNEVAFNNGSGSDGIDK---PIV 325
DB 436 NASEFQTHLFGYINYYTTSNLTWKNGVAFYSNNAQGGCKDKKEPIL 484

RESULT 13
US-10-378-674-4
; Sequence 4, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI
; FILE REFERENCE: P07566US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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; LENGTH: 343
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-4

Query Match          20.4%; Score 353; DB 15; Length 343;
Best Local Similarity 30.6%; Pred. No. 1.3e-21;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNTVGI-DSGTTYPHQAGYVKLNGFSPVNSAVKGDPTKIVPEKLNGLVTS 71
DB 247 VTQD--SITEGYDSDGIIKRAHDAENLIYDTEVEDDKVSGDTMTVINIDKNVPSDLTD 304
QY 72 TAKVPPIMAGD-OVLANGVID-SDGNVITYFTFYVNTKDDVKATLTPPAYIDPENVKKTG 129
DB 305 SFAIPKIKDNGSEIIAAGTVNTKQITFTFYVDVYKXENIKALKLTSYIDSKVYNNN 364
QY 130 ---NVTLATIGSTTAKTVLVDEKYGKFPNLSIKGTIDQIDKTNNTYRQTIYVNSGD 186
DB 365 TKLDVEYKTALS--VNKTIIVYQKPNENSTALQSMFTNIDTKNHTVEQTIYINFL-- 420
QY 187 NVIAPVLGNLKPNTSNAIDQNTSIKYKXVDNAADLESYFV--NPENFEDVINSVNI 245

RESULT 14
US-10-378-674-2
; Sequence 2, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI
; FILE REFERENCE: P07566US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-2

Query Match          20.4%; Score 353; DB 15; Length 560;
Best Local Similarity 30.6%; Pred. No. 2.8e-21;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNTVGI-DSGTTYPHQAGYVKLNGFSPVNSAVKGDPTKIVPEKLNGLVTS 71
DB 247 VTQD--SITEGYDSDGIIKRAHDAENLIYDTEVEDDKVSGDTMTVINIDKNVPSDLTD 304
QY 72 TAKVPPIMAGD-OVLANGVID-SDGNVITYFTFYVNTKDDVKATLTPPAYIDPENVKKTG 129
DB 305 SFAIPKIKDNGSEIIAAGTVNTKQITFTFYVDVYKXENIKALKLTSYIDSKVYNNN 364
QY 130 ---NVTLATIGSTTAKTVLVDEKYGKFPNLSIKGTIDQIDKTNNTYRQTIYVNSGD 186
DB 365 TKLDVEYKTALS--VNKTIIVYQKPNENSTALQSMFTNIDTKNHTVEQTIYINFL-- 420
QY 187 NVIAPVLGNLKPNTSNAIDQNTSIKYKXVDNAADLESYFV--NPENFEDVINSVNI 245

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Mon Mar 29 10:05:53 2004

us-10-056-052a-4.rapb

Page 8

Db 421 RYSAKETNNVNSGNGDEGSIIDSTIIKYYKVDNQLPDSNRIVYSEYEDVTNDYA 480
Qy 246 TFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 481 QLGNNNDVNNIFG---NIDSPYIIKVISKYDPN-KDDYTTIQQVYTMQTTINEYTG-- 533
Qy 299 WRSMSNDNEVAFNNNGSGSGDGIDKPYVPEQ 328
Db 534 FRTASYDNTIAFSTSSGQGG-DLP--PEK 560

RESULT 15
US-10-282-122A-70481
Sequence 70481, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 70481
LENGTH: 892
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70481

Query March 20:4%; Score 353; DB 12; Length 892;
Best Local Similarity 30.6%; Pred. No. 5.5e-21;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

Qy 13 ITNQLTNTVGI-DSGTTPVPHQAGYKLVNYSFVPSNPAVKGDTFKITVPEKELNGVTS 71
Db 246 VTDO-SITBEGYDSDGIRKHADELNIYDTFEVDKXKSGDPTMTVNIIDKNTVPSDLTD 303
Qy 72 TAKPPIIMAGD-QVLANGVID-SDGNVITFTDYVNTKDVKATLTMFAVIDPENVYKKG 129
Db 304 SFALPKIKDSGEIITAGTYDNTNKQITLYFTDYDKENTKAKLTKLSTIIDSXKVPNNN 363

Qy 130 --NVLATGISTTANKIVLVDEYKXKFNLSIGKTIIDQIKRNTTYRQTIYVNPSCD 186
Db 364 TKLDVEYKTALS--VNKTIIVEYQKNEENRNTANLSMFTNIDTKHATVEQTIYINPL-- 419
Qy 187 NVIAFVLGNLKPRTDSNALIDQONTSIKYYKVDNADLSSEYFV-NPENFEDVTSVNI 245
Db 420 RYSAKETNNVNSGNGDEGSIIDSTIIKYYKVDNQLPDSNRIVYSEYEDVTNDYA 479
Qy 246 TFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 480 QLGNNNDVNNIFG---NIDSPYIIKVISKYDPN-KDDYTTIQQVYTMQTTINEYTG-- 532
Qy 299 WRSMSNDNEVAFNNNGSGSGDGIDKPYVPEQ 328
Db 533 FRTASYDNTIAFSTSSGQGG-DLP--PEK 559

Search completed: March 26, 2004, 05:53:03
Job time : 1086.06 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:17 ; Search time 34.039 Seconds
(without alignments)
935.380 Million cell updates/sec

Title: US-10-056-052a-4

Perfect score: 1732

Sequence: 1 WVAADAPAPAGTDITNQLTNV.....NGSGSGDIDKPVVPEQPD 331

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1727	99.7	933	2 S41539	fibrinogen-binding
2	1517	87.6	989	2 D89852	fibrinogen-binding
3	416.5	24.0	961	2 G90053	hypothetical prote
4	409	23.6	940	2 S19702	fibrinectin-bindin
5	349	20.2	1092	2 T30214	fibrinogen-binding
6	331	19.1	1018	2 A32192	fibrinogen-binding
7	324.5	18.7	1038	2 H90053	hypothetical prote
8	323.5	18.7	1166	2 T28680	fibrinogen-binding
9	320.5	18.5	1141	2 E89824	hypothetical prote
10	312.5	18.0	877	2 P90070	clumping factor B
11	257.5	14.9	1315	2 T28679	fibrinogen-binding
12	240.5	13.9	1385	2 D89824	hypothetical prote
13	229.5	13.3	953	2 C89824	hypothetical prote
14	182	10.5	1039	2 T30856	protein F2 - Stre
15	161.5	9.3	463	2 AG1542	wall associated pr
16	157.5	9.1	462	2 AH1184	wall associated pr
17	147.5	8.5	586	2 AD1458	probable peptidogl
18	141	8.1	1386	2 AC1533	surface protein (l
19	137	7.9	439	2 AE1251	probable peptidogl
20	137	7.9	4152	2 T31102	filamentous hemag
21	135	7.8	1983	2 G86643	hypothetical prote
22	132.5	7.7	1457	2 D81019	adhesion and penet
23	132	7.6	1449	2 B81963	IGA-specific serin
24	129	7.4	762	2 A34355	cell surface prote
25	128	7.4	1158	2 AF1852	hypothetical prote
26	128	7.4	2021	2 A97859	190-kDa cell surfa
27	127	7.3	642	2 D81401	probable flagellar
28	127	7.3	793	2 AH1094	probable peptidogl
29	126.5	7.3	571	2 A11094	probable peptidogl

30	126.5	7.3	1029	2 T10852	outer membrane pro
31	124.5	7.2	1039	2 D97985	hypothetical prote
32	123.5	7.1	1417	2 AG2137	hypothetical prote
33	122.5	7.1	657	2 AD1525	probable cell surf
34	122.5	7.1	1039	2 H95115	conserved hypotnet
35	122.5	7.1	1487	2 AC2560	hypothetical prote
36	122	7.0	1578	2 AD1512	peptidoglycan bonu
37	121.5	7.0	2249	2 A41477	190K surface anti9
38	121.5	7.0	3890	2 C88921	hypothetical prote
39	121	7.0	1510	2 AF0394	probable adhesin h
40	119.5	6.9	691	2 B75622	hypothetical prote
41	119.5	6.9	836	2 D97182	extracellular neut
42	118.5	6.8	749	2 E86774	hypothetical prote
43	118.5	6.8	1369	2 T17504	hypothetical prote
44	118	6.8	1973	2 T10944	surface protein pr
45	117.5	6.8	449	2 UC7306	extracellular prot

ALIGNMENTS

RESULT 1

S41539
fibrinogen-binding protein - Staphylococcus aureus

N/Alternate names: clumping factor

C/Species: Staphylococcus aureus

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C/Accession: S41539; S36630

R/McDevitt, D.; Franco, P.; Vaudaux, P.; Foerster, T.J.

Mol. Microbiol. 11, 237-248, 1994

A/Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Staphylococcus aureus

A/Reference number: S41539; PMID:94224142; PMID:8170386

A/Accession: S41539

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1933 <MCD>

A/Cross-References: EMBL:218852; NID:G9397525; PIDN:CAA79304.1; PID:G9397526

Query Match 99.7%; Score 1727; DB 2; Length 933;
Best Local Similarity 100.0%; Pred. No. 1e-99;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	VAAADAPAGTDITNQLTNVVGIDSGTTPVPHAGYVKNLYGFSVNSAVKGTFFKITP 61
DB	221	VAAADAPAGTDITNQLTNVVGIDSGTTPVPHAGYVKNLYGFSVNSAVKGTFFKITP 280
QY	62	KEMLNNGVTSTAKVPIMAGDOVLANGVIDSDGNVITFTDYVNTKDYKATITMPAYID 121
DB	281	KEMLNNGVTSTAKVPIMAGDOVLANGVIDSDGNVITFTDYVNTKDYKATITMPAYID 340
QY	122	PENYKKTGNVTLAGISTTANKTVLVDEKYGKFNLSIKGIIIDDKNNTRYRQIIV 181
DB	341	PENYKKTGNVTLAGISTTANKTVLVDEKYGKFNLSIKGIIIDDKNNTRYRQIIV 400
QY	182	NPSGDNVIAPLTGNLKPNIDSNALIDQNTSIKIVYKVDNAADLSBSYFVNPENFEDVTN 241
DB	401	NPSGDNVIAPLTGNLKPNIDSNALIDQNTSIKIVYKVDNAADLSBSYFVNPENFEDVTN 460
QY	242	SVNITFPENQKYKEFTPDQITTPYIVVNGHIDNSKGDALRSTLYGNSNIITWS 301
DB	461	SVNITFPENQKYKEFTPDQITTPYIVVNGHIDNSKGDALRSTLYGNSNIITWS 520
QY	302	MSMDNEVAFNNGSGDIDKPVVPEQPD 331
DB	521	MSMDNEVAFNNGSGDIDKPVVPEQPD 550

RESULT 2

D89852
fibrinogen-binding protein A, clumping factor [imported] - Staphylococcus aureus (strain
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: D89852

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsutsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: D89852
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-989 <KUR>
A/Cross-references: GB:BA000018; PID:g13700678; PIDN:BA841975.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: cflA

Query Match 87.6%; Score 1517; DB 2; Length 989;
Best Local Similarity 87.3%; Pred. No. 1.3e-86;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTNLTNLTAVTGIDSGTYYPHQAGYKLNYSFVNSAVKGDTEKITVP 61
DB 221 VAADAPAGTDTNLTNLTAVTGIDSGTYYPHQAGYKLNYSFVNSAVKGDTEKITVP 280
QY 62 KEINLNGVTSTAKVPEIMAGDQVLAVGIDSGNVITFTDYVNTKDYKATLTPAYID 121
DB 281 KEINLNGVTSTAKVPEIMAGDQVLAVGIDSGNVITFTDYVNTKDYKATLTPAYID 340
QY 122 PENVKTKGNVTLATGISTANKTVLVYERKGFNLSTKGTIDIDIKNTNNTYRQTIY 181
DB 341 PENVKTKGNVTLATGISTANKTVLVYERKGFNLSTKGTIDIDIKNTNNTYRQTIY 400
QY 182 NPSGDNIAPVLTGNLKPNTDSNALIDQNTSISKYKVDNAADLSBSYFVNPENFEDVTN 241
DB 401 NPSGDNIAPVLTGNLKPNTDSNALIDQNTSISKYKVDNAADLSBSYFVNPENFEDVTN 460
QY 242 SVNTTFPNNOYKVEFNTPDQITPTIIVVNGHIDPNSGDIALSTLYGNSNITIMS 301
DB 461 QVRISFPNNOYKVEFNTPDQITPTIIVVNGHIDPNSGDIALSTLYGNSNITIMS 520
QY 302 MSWNEVAFNNSSGSGDIDKPVVPEQDE 331
DB 521 MSWNEVAFNNSSGSGDIDKPVVPEQDE 550

RESULT 3

990053
hypotheoretical protein fnbB [imported] - *Staphylococcus aureus* (strain N315)
C/Species: *Staphylococcus aureus*
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: G90053
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsutsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: G90053
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-961 <KUR>
A/Cross-references: GB:BA000018; PID:g13702452; PIDN:BA843593.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnbB

Query Match 24.0%; Score 416.5; DB 2; Length 961;

Best Local Similarity 29.1%; Pred. No. 3.2e-18;
Matches 101; Conservative 69; Mismatches 144; Indels 33; Gaps 9;

QY 2 VAADAPAGTDTNLTNLTAVTGIDSGTYYPHQAGYKLNYSFVNSAVKGDTEKITVP 57
DB 158 VAADAPAGTDTNLTNLTAVTGIDSGTYYPHQAGYKLNYSFVNSAVKGDTEKITVP 217

QY 58 ITVPKEINLNGVTSTAKVPEIMAGDQVLAVGIDSGNVITFTDYVNTKDYKATLTP 115
DB 218 ITVPKEINLNGVTSTAKVPEIMAGDQVLAVGIDSGNVITFTDYVNTKDYKATLTP 277
QY 116 MPAYIDPENVKTKGNVTLATGISTANKTVLVYERKGFNLSTKGTIDIDIKNTNNTYRQTIY 170
DB 278 MPAYIDPENVKTKGNVTLATGISTANKTVLVYERKGFNLSTKGTIDIDIKNTNNTYRQTIY 333
QY 171 TNNYTRQTIIVVNSGDNVITFTDYVNTKDYKATLTPAYID 230
DB 334 EKGKFSFAVYKPNQSLTSVYTGQVTSYGKSA---NNPVKVKHAGSDELAEVY 389
QY 231 V---NPNFEDVTNSVITFTDYVNTKDYKATLTPAYID 287
DB 390 AKDDTSEKFEDEVTEKVLSTNSGVTLLNGDLDN---SKDYVYKGEYQDNK---DLNFR 446
QY 288 STLYGNSNITIMR-----MSWNEVAFNNSSGSGDIDKPVVPEQDE 326
DB 447 THLSGYHKKYYPYYPYYPYYPVLTNNNGVAFYNNNAKGDGKRPNDP 493

RESULT 4

519702
fibronectin-binding protein B - *Staphylococcus aureus*
C/Species: *Staphylococcus aureus*
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999
C/Accession: S19702
R;Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A>Title: Two different genes encode fibronectin binding proteins in *Staphylococcus aureus*.
A/Reference number: S19702; MUID:92111475; PMID:1857266
A/Accession: S19702
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-940 <JOB>
A/Cross-references: EMBL:X62992; NID:g49040; PIDN:CAA44726.1; PID:g581562
C/Keywords: fibronectin binding

Query Match 23.6%; Score 409; DB 2; Length 940;
Best Local Similarity 28.9%; Pred. No. 9.2e-18;
Matches 101; Conservative 72; Mismatches 131; Indels 46; Gaps 11;

QY 2 VAADAPAGTDTNLTNLTAVTGIDSGTYYPHQAGYKLNYSFVNSAV 51
DB 155 VVEETKATGTDVTK-----VEVEGSEIVGHKQDTNWNHNAERTLTKKMFEGGK 209
QY 52 KQDTFKITVPKELNNGVTSTAKVPEIMAGDQVLAVGIDSGNVITFTDYVNTKDY 110
DB 210 AGDYFDTLSDNVETHGISTLRKYPEIKSTDGQVATGEIIGERKRVTFREYVQEKDL 269
QY 111 KATLMPAYIDPENVKTKGNVTLATGISTANKTVLVYERKGFNLSTKGTIDIDIKNTNNTYRQTIY 165
DB 270 TELSNNLEIDPTTYTGQNVQNVKLETTVSKTFNFIQYGVARDNG---VTANRI 325
QY 166 DOIDKTNNTYRQTIIVVNSGDNVITFTDYVNTKDYKATLTPAYID 221
DB 326 DTLNKVDGKFSFAVYKPNQSLTSVYTGQVTSYGKSA---NNPVKVKHAGSDELAEVY 377
QY 222 AADLSGYSFVNPEN---FEDVTNSVITFTDYVNTKDYKATLTPAYID 278
DB 378 SDDLAEVYAKDDVSKEDVDNNSLDPTDNGSYSLFNNLDQ---SKNYVYKGEYD 435
QY 279 NSKGDALASTLYGNSNITIMRMSWNEVAFNNSSGSGDIDKPVVPEQDE 325
DB 436 NALNLEFQTHLFGYNYVYTSNLTWKGVAFYNNNAOGDGKDLKEPIL 484

RESULT 5

T30214
fibronectin-binding protein - *Staphylococcus epidermidis*
C/Species: *Staphylococcus epidermidis*
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C/Accession: T30214

R.Josefsson, E.; McCrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T.
Microbiology 144, 3387-3395, 1998
A:Title: Three new members of the serine-aspartate repeat protein multi-gene family of St
A:Reference number: 220510; MUID:9998700; PMID:9884231
A:Accession: T28679
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1115 <JOS>
A:Cross-references: EMBL:AJ005646; NID:e1318791; PID:e1318792; PIDN:CAA0651.1
C:Genetics:
A:Gene: sdrD

Query Match 14.9%; Score 257.5; DB 2; Length 1315;
Best Local Similarity 26.1%; Pred. No. 3.8e-08;
Matches 88; Conservative 51; Mismatches 157; Indels 31; Gaps 12;

QY 13 ITNQLNVTGIDSGTTPVPHQAGYKLNKGFSVPSAVKGDTPKLTPEKLNLTNGVT-- 70
DB 251 ITSNTLTITVVDADKNNKIVPAQ-DYLSLKSQITVDKVSQDYFTIKXSDTYQVYGLNPE 309
QY 71 -----STAKVPIMAGDQVLANGVIDSGNVI-YFTDYVNTKDYKATLTMPAYIDPEN 124
DB 310 DIKNIDIDP---NNGETIATAKHDTANNLTITFTDYDRFNSQWGINYSIYMDADT 366
QY 125 VKKTGN-VTLATGIGSTTANKTVLVDEYKXKGFYNLSIGK---TIDQIDKTNNT--YRQ 177
DB 367 IPVSKVDVFNVTIGITTTKTANNIOPYVYVNEKKSISATETVSHVKNENGYKQ 426
QY 178 TIYVNSGDNVIAPIVTLNKLKPTDSNAL-IDQNTSIRKYKVDNADLSSEYFVNPEN 235
DB 427 TIYVNSNSLTKAKIKVQAYHSSYPNNIGQINKDVTDIKIYQVPGYTLNKGYVNTKE 486
QY 236 FEEDVNTSV--NITFPNQYKVEFNTPDQITPYIVVNGHID-PNSKGDALRSTLYG 292
DB 487 LNDVITQYQKITYGNNNSAVIDFGNAD---SAYVVMVNTKFOYTNSESPVLVQMATLS 542
QY 293 YNSNIIRSMWMDNEVAFNNGSGSGDG 319
DB 543 STGN---KSVSTGNALGFTNNGSGAG 566

RESULT 12

hypothetical protein sdrD [imported] - Staphylococcus aureus (strain N315)
D89824
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
A:Accession: D89824
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89824
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1385 <KUR>
A:Cross-references: GB:BA000018; PID:g13700454; PIDN:BA841751.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sdrD

Query Match 13.9%; Score 240.5; DB 2; Length 1385;
Best Local Similarity 26.1%; Pred. No. 4.7e-07;
Matches 86; Conservative 54; Mismatches 154; Indels 35; Gaps 14;

QY 13 ITNQLNVTGIDSGTTPVPHQAGYKLNKGFSVPSAVKGDTPKLTPEKLNLTNGVT-- 70
DB 251 ITSNTLTITVVDADKNNKIVPAQ-DYLSLKSQITVDKVSQDYFTIKXSDTYQVYGLNPE 309
QY 71 -----STAKVPIMAGDQVLANGVIDSGNVI-YFTDYVNTKDYKATLTMPAYIDPEN 124
DB 310 DIKNIDIDP---NNGETIATAKHDTANNLTITFTDYDRFNSQWGINYSIYMDADT 366

QY 125 V---KKTGNVTLATGISTTANKTVLVDEYKXKGFYNLSIGK---TIDQIDKTNNT--Y 175
DB 367 IPVSKR--DVPSVTLIGNQITTTTADITVPAYEADNNISGAFTEVSHVGNVEDPGYY 424
QY 176 RQTIYVNSGDNVI-APVLGNLKEPNTDSN-ALIDQNTSIRKYKVDNADLSSEYFVNP 233
DB 425 NQVYVNEPMDKDLKAKLKYEAHPKPTNIGQINQVNTNIKIYRPEGTLNKGIDVNT 484
QY 234 ENFEDVNTSV--NITFPNQYKVEFNTPDQITPYIVVNGHID-PNSKGDALRSTLY 290
DB 485 NDVDTVDFKNTKMTYGSNSQVNLDFG---DITSAYVVMVNTKFOYTNSESPVLVQMAT 540
QY 291 YGNSNIIRSMWMDNEVAFNNGSGSGDG 319
DB 541 LSSTGN---KSVSTGNALGFTNNGSGAG 566

RESULT 13

hypothetical protein sdrC [imported] - Staphylococcus aureus (strain N315)
C89824
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
A:Accession: C89824
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89824
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-953 <KUR>
A:Cross-references: GB:BA000018; PID:g13700453; PIDN:BA841750.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sdrC

Query Match 13.3%; Score 229.5; DB 2; Length 953;
Best Local Similarity 24.9%; Pred. No. 1.4e-06;
Matches 84; Conservative 56; Mismatches 157; Indels 41; Gaps 12;

QY 6 AAPAGDITNQL--TNVTGIDSG-----TTVPYPHQAGYKLNKGFSVPSAVKGD 55
DB 178 APQGGTWNVDKRVHPTNIDIDKGVNKTGNTGFMTSDVLTAKMYTIDSVKSGDT 237
QY 56 FKIVPEKLNLTNGVTSNAKVPIM-AGDQVLANGVIDSGN-VIYFTDYVNTKDYKAT 113
DB 238 FTFYGGQFPPGSRVLPDSQTNLNAQGNITAKGIYDSKNTTITTYTINVDQYTNVSGS 297
QY 114 LTMAYIDPEN--VKKTG---NVTLATGISTTANKTVLVDEYKXKGFYNLSIGKTIQI 168
DB 298 FEQVAFKREKATDKIAYKAEVTL---GNDTYSKVIDYGNQKQQLISSTNYINNE 353
QY 169 DKTNNYRQTIYVNSGDNVIAPIVTLGNL--KPTDSNALIDQNTSIRKYKVDNADL 225
DB 354 DLSNR--MTYVAVQPKKYTKETFTNLGYKFNPAK-----NFKIYETIDNOF 402
QY 226 SESYFVNEFEDVNTSVNITFPNPNQ--KYVEFNTPDQITPYIVVNGHIDPNSKGL 284
DB 403 VDSFTPDSKLDVTDGQFDVYISNDNNTATVLDLNGSSDSKQYIIQVAVPDMSTDNG 462
QY 285 ALRSTLYGNSNIIRSMWMDNEVAFNNGSGSGGIDIK 322
DB 463 KIDYLETONG-----KSSWSNSYSNVNGSSTANGDOK 495

RESULT 14

protein P2 - Streptococcus pyogenes
J30856
C:Species: Streptococcus pyogenes
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:50:40 ; Search time 125.592 Seconds
(without alignments)
744.658 Million cell updates/sec

Title: US-10-056-052a-4
Perfect score: 1732
Sequence: 1 WVAADAPAGATDITNQLTNV.....NGSGSGGDCIDKPVPEPDDE 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq.29Jan04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1732	100.0	331	5	AAE29263 Staphyloc
2	1732	100.0	345	2	AAW31555 Fibrinect
3	1727	99.7	520	5	AAE29262 Staphyloc
4	1727	99.7	933	3	AAE58435 Staphyloc
5	1727	99.7	933	4	AAE69508 Staphyloc
6	1723	99.5	927	2	ABM72221 Staphyloc
7	1723	99.5	927	2	AAW89801 Staphyloc
8	1723	99.5	936	2	AAW89801 Staphyloc
9	1518	87.6	1021	4	AAU33975 Staphyloc
10	1518	87.6	1021	4	AAU36951 Staphyloc
11	1517	87.6	935	6	ABU16402 Protein e
12	1433	82.7	496	6	AAU75490 S. aureus
13	1433	82.7	496	6	ADA89664 Staphyloc
14	1433	82.7	496	6	ADA89663 Staphyloc
15	416.5	24.0	961	6	ABU15854 Protein e
16	409	23.6	767	4	AAU34403 Staphyloc
17	409	23.6	767	4	AAU37547 Staphyloc
18	409	23.6	940	2	AAU37547 Fibrinect
19	409	23.6	940	6	ABU19111 Pathogen
20	409	23.6	948	6	ADA89470 Staphyloc
21	409	23.6	948	6	ABU18923 Pathogen
22	409	23.6	948	6	ABM72536 Staphyloc
23	353	20.4	343	7	ABM79016 Staphyloc
24	353	20.4	343	7	ABM79016 Staphyloc
25	353	20.4	892	6	ABU42557 Protein e

26	353	20.4	930	5	ABE40469 Staphyloc
27	353	20.4	991	3	AAW83171 Cell wall
28	353	20.4	991	3	AAW70120 Staph. ep
29	349	20.2	549	7	ABM79020 Staphyloc
30	349	20.2	1092	2	AAW41602 Staphyloc
31	349	20.2	1092	7	ABM79019 Staphyloc
32	346	20.0	978	4	AAU33960 Staphyloc
33	346	20.0	1001	4	AAU37093 Staphyloc
34	339	19.6	1018	4	AAU37245 Staphyloc
35	339	19.6	1018	4	AAU34301 Staphyloc
36	339	19.6	1018	6	ABU18922 Pathogen
37	331	19.1	1018	6	AAW82115 Fibrinect
38	331	19.1	1018	6	AAW82537 Staphyloc
39	331	19.1	1027	2	AAW89806 Staphyloc
40	324.5	18.7	1038	6	ABU15903 Protein e
41	323.5	18.7	1166	2	AAW8643 S. aureus
42	323.5	18.7	1166	6	ABU18982 Protein e
43	320.5	18.5	1141	6	ABU42327 Protein e
44	312.5	18.0	567	6	ADA89555 Staphyloc
45	312.5	18.0	743	6	ADA89690 Staphyloc

ALIGNMENTS

RESULT 1
ID AAE29263 standard; protein; 331 AA.
AC AAE29263;
XX
XX 27-JAN-2003 (first entry)
XX
XX Staphylococcus aureus Clf33 protein.
DE
XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
XX Staphylococcus aureus.
XX
XX WO200272600-A2.
XX
XX 19-SEP-2002.
XX
XX 28-JAN-2002; 2002WO-US002296.
XX
XX 26-JAN-2001; 2001US-0264072P.
XX 12-MAR-2001; 2001US-0274611P.
XX 18-JUN-2001; 2001US-0298413P.
XX 30-JUL-2001; 2001US-0308116P.
XX
XX (INHI-) INHIBITEX INC.
XX
XX Patcl JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX WPI: 2002-759834/82.
XX N-PSDB; AAD46862.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
XX treating or preventing Staphylococcus aureus infection e.g. wound
XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
XX a human or animal.
XX
XX Claim 9; Page 70-72; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
XX factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
XX monoclonal antibody is useful for treating or preventing S. aureus
XX infection in a human or animal, and for inhibiting the binding of
XX staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
XX S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
XX protein is useful for inducing an immunological response in a human or

CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus Clf33 protein

XX Sequence 331 AA;

Query Match 100.0%; Score 1732; DB 5; Length 331;
Best Local Similarity 100.0%; Pred. No. 2,2e-116;

Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAADAPAACTDITNOLNTVAVGIDSGTTPYPHQAGYVKNLNGFSPNSAVKGDTEKITV 60
DB 1 MVAADAPAACTDITNOLNTVAVGIDSGTTPYPHQAGYVKNLNGFSPNSAVKGDTEKITV 60
QY 61 PRELNNGVTSTAKVPPIAGDQVLAVNGVIDSDGNVITFTDYVNTKDVKATLTMPAYI 120
DB 61 PRELNNGVTSTAKVPPIAGDQVLAVNGVIDSDGNVITFTDYVNTKDVKATLTMPAYI 120
QY 121 DPENVKKTGNVTLATGISTTANKTVLVDEYKGFNLSIKGTIDQIDKNNNTYRQITV 180
DB 121 DPENVKKTGNVTLATGISTTANKTVLVDEYKGFNLSIKGTIDQIDKNNNTYRQITV 180
QY 181 VNPSGDNVIAEVLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVT 240
DB 181 VNPSGDNVIAEVLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVT 240
QY 241 NSVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIIMR 300
DB 241 NSVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIIMR 300
QY 301 SMSWNEVAFPNNGSGSDGIDKPVVPEQDPE 331
DB 301 SMSWNEVAFPNNGSGSDGIDKPVVPEQDPE 331

RESULT 2

AAW31555 standard; protein; 345 AA.

XX AAW31555;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 21-MAY-1998 (first entry)

DE Fibronectin-binding MSCRAMM derivative pcf33.

XX Fibronectin; pcf33; collagen binding protein; sepsis; infection;
XX microbial surface component recognising adhesive molecule; MSCRAMM;
XX adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Peptide 1..12

XX /note= "vector pQE30-derived peptide"

XX MO9743314-A2.

XX 20-NOV-1997.

XX 14-MAY-1997; 97WC-US008210.

XX 16-MAY-1996; 96US-0017678P.

XX (TEXA-) UNITV TEXAS A & M SYSTEM.

XX (UABR-) UAB RES FOUND.

XX Hoecek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;

XX WPI, 1998-008801/01.

XX Antibody that interacts with collagen binding domain of Staphylococcal

PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.

XX Disclosure; Page 91; 143pp; English.

XX This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component recognising adhesive matrix molecule (MSCRAMM)
CC derivative pcf33, plus a vector-derived N-terminal peptide. The invention
CC relates to claimed nucleic acid sequences (see AAT93435-38) encoding S.
CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC AAW31552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. pcf33 and pQD (see AAW31556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)

XX Sequence 345 AA;

Query Match 100.0%; Score 1732; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 2,4e-116;

Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAADAPAACTDITNOLNTVAVGIDSGTTPYPHQAGYVKNLNGFSPNSAVKGDTEKITV 60
DB 13 MVAADAPAACTDITNOLNTVAVGIDSGTTPYPHQAGYVKNLNGFSPNSAVKGDTEKITV 72
QY 61 PRELNNGVTSTAKVPPIAGDQVLAVNGVIDSDGNVITFTDYVNTKDVKATLTMPAYI 120
DB 73 PRELNNGVTSTAKVPPIAGDQVLAVNGVIDSDGNVITFTDYVNTKDVKATLTMPAYI 132
QY 121 DPENVKKTGNVTLATGISTTANKTVLVDEYKGFNLSIKGTIDQIDKNNNTYRQITV 180
DB 133 DPENVKKTGNVTLATGISTTANKTVLVDEYKGFNLSIKGTIDQIDKNNNTYRQITV 192
QY 181 VNPSGDNVIAEVLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVT 240
DB 193 VNPSGDNVIAEVLGNLKPNTDSNALIDQNTSISKYKVDNAADLSSEYFVNPENFEDVT 252
QY 241 NSVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIIMR 300
DB 253 NSVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIIMR 312
QY 301 SMSWNEVAFPNNGSGSDGIDKPVVPEQDPE 331
DB 313 SMSWNEVAFPNNGSGSDGIDKPVVPEQDPE 343

RESULT 3

AAE29262 standard; protein; 520 AA.

XX AAE29262;

XX 27-JAN-2003 (first entry)

XX Staphylococcus aureus Clf40 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX MO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WC-US002236.


```

XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.
XX
XX (INHIBITEX INC.
XX
XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
XX WPI; 2002-759634/82.
XX N-PSDB; AAD46861.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
XX treating or preventing Staphylococcus aureus infection e.g. wound
XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
XX a human or animal.
XX
XX Claim 9; Page 67-69; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
XX factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
XX monoclonal antibody is useful for treating or preventing S. aureus
XX infection in a human or animal, and for inhibiting the binding of
XX Staphylococcus aureus to fibrinogen or fibrin. The immunogenic fragment
XX S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
XX protein is useful for inducing an immunological response in a human or
XX animal. These staphylococcal infections include wound infections, sepsis,
XX impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
XX present sequence is Staphylococcus aureus Clf40 protein.
XX
XX Sequence 520 AA;
XX
XX
XX Query Match 99.7%; Score 1727; DB 5; Length 520;
XX Best Local Similarity 100.0%; Pred. No. 9.2e-116;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 VAADAPAAAGTIDITNQLNTNTVIGIDSGTTPYPHQAGYVKLVGSPVNSAVKGDFTKTIYP 61
XX 182 VAADAPAAAGTIDITNQLNTNTVIGIDSGTTPYPHQAGYVKLVGSPVNSAVKGDFTKTIYP 241
XX
XX 62 KELNNGVTSKAPKPIIMAGDQVLANGVSDGNVITFTDYNTKDVKATLTMPIYID 121
XX 242 KELNNGVTSKAPKPIIMAGDQVLANGVSDGNVITFTDYNTKDVKATLTMPIYID 301
XX
XX 122 PENVKKTGNVTLATIGSTTANKTVLVDEYKGYKFNLSIKGTIDQIDKNTNTYRQTIYV 181
XX 302 PENVKKTGNVTLATIGSTTANKTVLVDEYKGYKFNLSIKGTIDQIDKNTNTYRQTIYV 361
XX
XX 182 NPSGDVIAPIVLTGNLKNPTDSNALIDQONTISKYKVNADLSSYVFNENFEDVTN 241
XX 362 NPSGDVIAPIVLTGNLKNPTDSNALIDQONTISKYKVNADLSSYVFNENFEDVTN 421
XX
XX 242 SVNITFPNPNQYKVEFNTPDDQITTPYIVVNGHIDPNKSKDLARSTLYGNSNIWRS 301
XX 422 SVNITFPNPNQYKVEFNTPDDQITTPYIVVNGHIDPNKSKDLARSTLYGNSNIWRS 481
XX
XX 302 MSMDNEVAFNNGSGSDGIDKPIVPEQDPE 331
XX 482 MSMDNEVAFNNGSGSDGIDKPIVPEQDPE 511
XX
XX
XX RESULT 4
XX ID AAY58435
XX AC AAY58435;
XX
XX 27-MAR-2000 (first entry)
XX
XX Staphylococcus aureus fibrinogen binding ClfA protein.
XX
XX ClfA, fibrinogen binding protein; bacterial colonisation;

```

```

XX indwelling medical device; staphylococcal infection.
XX
XX OS Staphylococcus aureus.
XX
XX Key Location/Qualifiers
XX Peptide 1..39
XX /note="Signal peptide"
XX Region 40..559
XX /note="Region A"
XX Region 332..550
XX /note="Fibrinogen-binding region"
XX Region 560..867
XX /note="Region R"
XX Region 896..900
XX /note="Gram positive wall-associated consensus motif"
XX
XX US6008341-A.
XX
XX 28-DEC-1999.
XX
XX 22-AUG-1994; 94US-00293728.
XX
XX 22-AUG-1994; 94US-00293728.
XX
XX (QUEEN-) QUEEN ELIZABETH COLLEGE DUBLIN.
XX
XX Foster TV, McDevitt DL;
XX
XX WPI; 2000-096389/08.
XX N-PSDB; AAZ55832.
XX
XX Nucleic acid encoding the fibrinogen-binding protein of Staphylococcus
XX aureus, useful for treatment or prevention of infections.
XX
XX Disclosure; Fig 2A-1-4; 35pp; English.
XX
XX This sequence represents the Staphylococcus aureus fibrinogen-binding
XX protein, ClfA. ClfA is an important receptor involved in S. aureus
XX colonisation of indwelling medical devices (e.g., catheters, artificial
XX heart valves). Shortly after implantation, the surfaces of medical
XX devices become coated with host plasma and matrix proteins such as
XX fibrinogen and fibronectin, and there is considerable evidence to suggest
XX that bacterial adherence to fibrinogen/fibrin is important in the
XX initiation of device-related infection. The fibrinogen-binding region of
XX ClfA is thought to reside between residues 332 and 550 in a region
XX comprising 154 repeats of the dipeptide Ser-Asp, and the C-terminus
XX contains features present in surface proteins of other Gram positive
XX bacteria that are responsible for anchoring the protein to the cell wall
XX and cell membrane. ClfA, or its fragments, may be used to block S. aureus
XX colonisation of wounds, to prevent adherence of S. aureus to indwelling
XX medical devices, as vaccines to protect against S. aureus infection
XX (e.g., mastitis in ruminants), to raise specific antibodies, and for
XX diagnosis (by agglutination or immunoassay). The specific antibodies are
XX used for passive immunisation, to block infection of wounds or adhesion
XX of S. aureus and for diagnosis. Nucleotides encoding ClfA and its
XX fragments may be used as diagnostic probes
XX
XX Sequence 933 AA;
XX
XX
XX Query Match 99.7%; Score 1727; DB 3; Length 933;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-115;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 VAADAPAAAGTIDITNQLNTNTVIGIDSGTTPYPHQAGYVKLVGSPVNSAVKGDFTKTIYP 61
XX 221 VAADAPAAAGTIDITNQLNTNTVIGIDSGTTPYPHQAGYVKLVGSPVNSAVKGDFTKTIYP 280
XX
XX 62 KELNNGVTSKAPKPIIMAGDQVLANGVSDGNVITFTDYNTKDVKATLTMPIYID 121
XX 281 KELNNGVTSKAPKPIIMAGDQVLANGVSDGNVITFTDYNTKDVKATLTMPIYID 340
XX
XX 122 PENVKKTGNVTLATIGSTTANKTVLVDEYKGYKFNLSIKGTIDQIDKNTNTYRQTIYV 181

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Db 341 PENVKKTGNVTLTATGISTANKTVLDYERKGFNLSIKGTIDIDKTNNTYRQTIIV 400
Qy 182 NPSGDVNIAPVLTGNLKPNTDSNALIDQNTSIRKTVKVDNAADLSSEYFNPENFEDVTN 241
Db 401 NPSGDVNIAPVLTGNLKPNTDSNALIDQNTSIRKTVKVDNAADLSSEYFNPENFEDVTN 460
Qy 242 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDALALRSTLYGNSNIITRS 301
Db 461 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDALALRSTLYGNSNIITRS 520
Qy 302 MSMDNEVAFNNGSGSGDIDKPVVPEQPD 331
Db 521 MSMDNEVAFNNGSGSGDIDKPVVPEQPD 550

```

RESULT 5

AAB69508
ID AAB69508 standard; protein; 933 AA.

XX AAB69508;

DT 23-APR-2001 (first entry)

DE Staphylococcus aureus ClfA protein.

XX Staphylococcus aureus; ClfA; antibiotic; vaccine;
KM fibrinogen binding protein; bacterial infection; mastitis.

OS Staphylococcus aureus.

PN US6177084-B1.

PD 23-JAN-2001.

PF 19-OCT-1999; 99US-00421868.

PR 22-AUG-1994; 94US-00293728.

PA (QUEEN-) QUEEN ELIZABETH COLLEGE DUBLIN.

PI Foster TJ, McDevitt DJ;

DR WPI; 2001-181608/18.

DR N-PSDB; AAF58593.

XX Novel Staphylococcus aureus fibrinogen binding protein useful as vaccine
PT to prevent infection, promote wound healing, block adherence to
PT indwelling medical devices and for diagnosing staphylococcus aureus
PT infection.

PS Claim 5; Fig 2; 30pp; English.

XX The present sequence is a novel Staphylococcus aureus fibrinogen binding
CC protein. It is useful as a vaccine to protect against human and animal
CC infections caused by S.aureus, such as against mastitis, to block
CC S.aureus from colonising and infecting a wound, to block adherence of
CC S.aureus to indwelling medical devices such as catheters, replacement
CC heart valves and cardiac assist devices. The protein can be used to
CC diagnose bacterial infections. Polyclonal and monoclonal antibodies
CC raised against the fibrinogen binding protein are useful for passively
CC immunising against infections caused by S.aureus, to prevent infection of
CC a wound and to diagnose bacterial infections

XX Sequence 933 AA;

XX Query Match 99.7%; Score 1727; DB 4; Length 933;

XX Best Local Similarity 100.0%; Pred. NO. 1.9e-115;

XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAADAPAAAGTDTITNLTNTVTVGIDSGTTVPYHQAQYVLTANVGFVSPNSAVKGTFTKIVP 61
Db 221 VAADAPAAAGTDTITNLTNTVTVGIDSGTTVPYHQAQYVLTANVGFVSPNSAVKGTFTKIVP 280

```

Qy 62 KELNNGVTSAPKVPPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVAKALLTMPAYID 121
Db 281 KELNNGVTSAPKVPPIIMAGDQVLANGVIDSDGNVITFTDYVNTKDVAKALLTMPAYID 340
Qy 122 PENVKKTGNVTLTATGISTANKTVLDYERKGFNLSIKGTIDIDKTNNTYRQTIIV 181
Db 341 PENVKKTGNVTLTATGISTANKTVLDYERKGFNLSIKGTIDIDKTNNTYRQTIIV 400
Qy 182 NPSGDVNIAPVLTGNLKPNTDSNALIDQNTSIRKTVKVDNAADLSSEYFNPENFEDVTN 241
Db 401 NPSGDVNIAPVLTGNLKPNTDSNALIDQNTSIRKTVKVDNAADLSSEYFNPENFEDVTN 460
Qy 242 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDALALRSTLYGNSNIITRS 301
Db 461 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDALALRSTLYGNSNIITRS 520
Qy 302 MSMDNEVAFNNGSGSGDIDKPVVPEQPD 331
Db 521 MSMDNEVAFNNGSGSGDIDKPVVPEQPD 550

```

RESULT 6

ABJ18947
ID ABJ18947 standard; protein; 933 AA.

XX ABJ18947;

DT 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 93.

XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;

KM hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;

KM auto-immunity; vaccine; staphylococcal infection; antibody; cancer;

XX autoimmune disease; HIV; hepatitis.

OS Staphylococcus sp.

PN WO200259148-A2.

PD 01-AUG-2002.

PF 21-JAN-2002; 2002WO-EP000546.

PR 26-JAN-2001; 2001AT-00000130.

PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

PI Weinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W,

PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichart T, Haefner M,

PI Tempelmeier B;

DR WPI; 2003-075410/07.

XX Identifying, isolating and producing hyperimmune serum-reactive antigens

XX from a pathogen, for preparing vaccine or medicament for treating or

XX preventing e.g. staphylococcal infections, comprises providing antibody

XX preparation.

XX Example 7; Page 160; 252pp; English.

XX The invention relates to a novel method for identifying, isolating and

XX producing hyperimmune serum-reactive antigens from a pathogen, tumour,

XX allergen, a tissue or host prone to auto-immunity, where the antigens are

XX used in a vaccine, comprises providing antibody preparation from a plasma

XX pool of a type of animal, or individual sera with antibodies against the

XX specific pathogen, tumour, allergen, tissue or host prone to auto-

XX immunity. The hyperimmune serum-reactive antigens comprising any of the

XX 62 sequences of 33-2261 amino acids fully defined in the specification,

XX or their hyperimmune fragments are useful for the manufacture of a

XX pharmaceutical preparation, particularly a vaccine against staphylococcal

XX infections or colonisation against S. aureus or S. epidermidis. The

CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against *S. aureus* or *S. epidermidis*. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX

Sequence 933 AA:

Query Match 99.7%; Score 1727; DB 6; Length 933;
Best Local Similarity 100.0%; Pred. No. 1,9e-115; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAAAGTDTITNQLINVTVGIDSGTTPYPHQAGYVKLYGFSVPSNAVKGDTEKTIYP 61
DB 221 VAADAPAAAGTDTITNQLINVTVGIDSGTTPYPHQAGYVKLYGFSVPSNAVKGDTEKTIYP 280
QY 62 KEINLNGVTSIAKVPPIAGDOVLANGVIDSDGNVITFTDYVNTKDDVKATLMPAYID 121
DB 281 KEINLNGVTSIAKVPPIAGDOVLANGVIDSDGNVITFTDYVNTKDDVKATLMPAYID 340
QY 122 PENVAKTGNVTLATIGSTTANKTVLDYEKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVAKTGNVTLATIGSTTANKTVLDYEKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAVLTGNLKEPNTDSNALIDQNTSIKYKVDNAADLSSESYFVNEPEDEDVTN 241
DB 401 NPSGDNVIAVLTGNLKEPNTDSNALIDQNTSIKYKVDNAADLSSESYFVNEPEDEDVTN 460
QY 242 SVNITFPENQYKVEFNPDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 461 SVNITFPENQYKVEFNPDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 520
QY 302 MSWDNEVAFNNNGSGSGDIDKPYVPEQDPE 331
DB 521 MSWDNEVAFNNNGSGSGDIDKPYVPEQDPE 550

RESULT 7

ABM72221
ID ABM72221 standard; protein; 927 AA.

XX ABM72221;
XX
XX 20-NOV-2003 (first entry)
XX
XX Staphylococcus aureus protein #1461.
XX
XX Staphylococcus aureus protein #1461.
XX
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX
XX enzymatic assay; antibiotic target.
XX
XX Staphylococcus aureus.
XX
XX WO200294868-A2.
XX
XX 28-NOV-2002.
XX
XX 27-MAR-2002; 2002WO-IB002637.
XX
XX 27-MAR-2001; 2001GB-00007661.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Masignani V, Mora M, Scarselli M;
XX
XX WPI; 2003-120786/11.
XX
XX N-PSDB; ACF73781.
XX
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX preventing staphylococcal infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX
XX

XX
XX Claim 1, SEQ ID NO 2922; 49pp; English.

XX The invention relates to novel genes and encoded proteins from.
XX Staphylococcus aureus. A composition comprising the *S. aureus* protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to Staphylococcus bacteria, specifically an
XX infection caused by *S. aureus*. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel *S. aureus* proteins of the invention
XX

Sequence 927 AA:

Query Match 99.5%; Score 1723; DB 6; Length 927;
Best Local Similarity 99.7%; Pred. No. 3.7e-115; Indels 0; Gaps 0;
Matches 329; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAADAPAAAGTDTITNQLINVTVGIDSGTTPYPHQAGYVKLYGFSVPSNAVKGDTEKTIYP 61
DB 221 VAADAPAAAGTDTITNQLINVTVGIDSGTTPYPHQAGYVKLYGFSVPSNAVKGDTEKTIYP 280
QY 62 KEINLNGVTSIAKVPPIAGDOVLANGVIDSDGNVITFTDYVNTKDDVKATLMPAYID 121
DB 281 KEINLNGVTSIAKVPPIAGDOVLANGVIDSDGNVITFTDYVNTKDDVKATLMPAYID 340
QY 122 PENVAKTGNVTLATIGSTTANKTVLDYEKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVAKTGNVTLATIGSTTANKTVLDYEKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAVLTGNLKEPNTDSNALIDQNTSIKYKVDNAADLSSESYFVNEPEDEDVTN 241
DB 401 NPSGDNVIAVLTGNLKEPNTDSNALIDQNTSIKYKVDNAADLSSESYFVNEPEDEDVTN 460
QY 242 SVNITFPENQYKVEFNPDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 461 SVNITFPENQYKVEFNPDDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 520
QY 302 MSWDNEVAFNNNGSGSGDIDKPYVPEQDPE 331
DB 521 MSWDNEVAFNNNGSGSGDIDKPYVPEQDPE 550

RESULT 8

AAW89801
ID AAW89801 standard; protein; 936 AA.

XX AAW89801;
XX
XX 16-MAR-1999 (first entry)
XX
XX Staphylococcus aureus protein SEQ ID #5249.
XX
XX Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
XX
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX
XX skin infection; surgical wound infection; scalded skin syndrome;
XX
XX toxic shock syndrome.
XX
XX Staphylococcus aureus.
XX
XX EP786519-A2.
XX
XX 30-JUL-1997.
XX
XX 07-JAN-1997; 97EP-00100117.
XX
XX 05-JAN-1996; 96US-0009861P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX
XX

```

XX DR WPI; 1997-374922/35.
XX PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX PT stored on computer readable medium and used in the production of anti-
XX PT S.aureus vaccines.
XX PS Claim 23; Page 3255-3258; 3271PP; English.
XX CC This sequence represents a Staphylococcus aureus protein sequence of the
XX CC invention. The DNA sequences encoding the S.aureus proteins are recorded
XX CC on a computer readable medium, preferably selected from a floppy or hard
XX CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
XX CC Homology searches using the S.aureus DNA sequences allows putative
XX CC functions to be assigned so that protein-encoding or regulatory regions
XX CC of commercial, therapeutic or industrial importance can be obtained.
XX CC Specifically, sequences which are likely to encode antigens have been
XX CC identified and these polypeptides can be used in a vaccine composition
XX CC against S.aureus infection. The polypeptides can also be used in a kit
XX CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
XX CC in numerous human diseases, including cellulitis, eyelid infections, food
XX CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
XX CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
XX CC DNA sequences can be used for recombinant production of the polypeptides.
XX CC The new DNA sequences (and their fragments) are useful as primers or
XX CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
XX CC contained on the computer readable medium
XX SQ Sequence 936 AA;
XX
XX Query Match 99.5%; Score 1733; DB 2; Length 936;
XX Best Local Similarity 99.7%; Pred. No. 3,8e-115;
XX Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2 VAADAPAGAGDITNOLNTNVTGIDSGTTPYHQAGYKXNKGFSVNSAVKGPTEKITVP 61
DB 230 VAADAPAGAGDITNOLNTNVTGIDSGTTPYHQAGYKXNKGFSVNSAVKGPTEKITVP 269
QY 62 KEINLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVITFTDYNTKDDVAKLTMPAYID 121
DB 290 KEINLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVITFTDYNTKDDVAKLTMPAYID 349
QY 122 PENVKKTGNVTLATIGSTTANKTVLVYKEKGFYNLSIKGTTIDQDKTNNTYRQTIYV 181
DB 350 PENVKKTGNVTLATIGSTTANKTVLVYKEKGFYNLSIKGTTIDQDKTNNTYRQTIYV 409
QY 182 NPSGDNVIAPLVTGNLKNTDSNALIDQNTSISKYKVDNAADLSSESYFVNPNEDVTN 241
DB 410 NPSGDNVIAPLVTGNLKNTDSNALIDQNTSISKYKVDNAADLSSESYFVNPNEDVTN 469
QY 242 SVNITFPNPNQYKVEFTPDQDITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 470 SVNITFPNPNQYKVEFTPDQDITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 529
QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQDE 331
DB 530 MSWDNEVAFNNGSGSGDIDKPVVPEQDE 559
XX
XX RESULT 9
XX AAU33975
XX ID AAU33975 standard; protein; 1021 AA.
XX AC AAU33975;
XX
XX 14-FEB-2002 (first entry)
XX
XX Staphylococcus aureus cellular proliferation protein #251.
XX
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX antibacterial; drug design.
XX
XX Staphylococcus aureus.
XX
OS

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XX PN W0200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX 23-MAR-2000; 2000US-0206848P.
XX 26-MAY-2000; 2000US-0207727P.
XX 23-OCT-2000; 2000US-0242578P.
XX 27-NOV-2000; 2000US-0253625P.
XX 22-DEC-2000; 2000US-0257931P.
XX 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AAS51834.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5471; slimp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1021 AA;
XX
XX Query Match 87.6%; Score 1518; DB 4; Length 1021;
XX Best Local Similarity 87.3%; Pred. No. 2,3e-100;
XX Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
XX
QY 2 VAADAPAGAGDITNOLNTNVTGIDSGTTPYHQAGYKXNKGFSVNSAVKGPTEKITVP 61
DB 221 VAADAPAGAGDITNOLNTNVTGIDSGTTPYHQAGYKXNKGFSVNSAVKGPTEKITVP 280
QY 62 KEINLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVITFTDYNTKDDVAKLTMPAYID 121
DB 281 KEINLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVITFTDYNTKDDVAKLTMPAYID 340
QY 122 PENVKKTGNVTLATIGSTTANKTVLVYKEKGFYNLSIKGTTIDQDKTNNTYRQTIYV 181
DB 341 PENVKKTGNVTLATIGSTTANKTVLVYKEKGFYNLSIKGTTIDQDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPLVTGNLKNTDSNALIDQNTSISKYKVDNAADLSSESYFVNPNEDVTN 241
DB 401 NPSGDNVIAPLVTGNLKNTDSNALIDQNTSISKYKVDNAADLSSESYFVNPNEDVTN 460
QY 242 SVNITFPNPNQYKVEFTPDQDITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 301
DB 461 QVRISFPNPNQYKVEFTPDQDITTPYIVVNGHIDPNSKGLALRSTLYGNSNIIMRS 520

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302 MSWDNEVAFNNNGSGSDGIDKEPVPEQDE 331
 521 MSWDNEVAFNNNGSGSDGIDKPVPEQDE 550
 Db

RESULT 10
 ID AU36951 standard; protein; 1021 AA.
 AU36951
 AC AAU36951;
 DT 14-FEB-2002 (first entry)
 DE Staphylococcus aureus cellular proliferation protein #1121.
 KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 OS Staphylococcus aureus.
 PN MO200170955-A2.
 PD 27-SEP-2001.
 PF 21-MAR-2001; 2001MO-US009180.
 PP 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207272P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
 P1 Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS54810.
 XX
 PT New polynucleotides for the identification and development of
 FT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 12544; 511bp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes,
 CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 1021 AA;

Query Match 87.6%; Score 1518; DB 4; Length 1021;
 Best Local Similarity 87.3%; Pred. No. 2, 3e-100;
 Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0

2 VAADPAAGTDTTNTGAVIDSGTIVYPHQAGYVKLNTGFSVNSAIVKQDTRFTIVP 61

Dd		221	VADDAAPAGGDIINQIIDLIVKVTIIIDSGTYYPHQAGYVKLNIGSVPSAAYKGDTFKITVP	280
Qy		62	KEINLNGVSTAKVPPIMAGDQVLANGVIDSDGNVIYTFPDYNNTKDDYKAILTMPAYID	121
Dd		281	KEINLNGVSTAKVPPIMWGDQVLANGVIDSDGNVIYTFPDYNTKENVTANITMPAYID	340
Qy		122	PENVKKGTANTLTAGISGTANKTVLDYKRYGKFYNLSIKGTIDQIDKTNNTRYQRIYV	181
Dd		341	PENVTKGTANTLTITTGISTNTASKTVLIDYKRGFHNLSIKGTIDQIDKTNNTRYQRIYV	400
Qy		182	NPGSDNVAIEVLGTNLKNPTDSNALIDQONTSIKVYRVNDAAIDLESYFYVNPFEDVTN	241
Dd		401	NPGSDNVVLPAIIGNLIIPNTRKSNAIIDAKOTDIKYAVRDNANDISESYVNPSPFEDVTN	460
Qy		242	SVNITFPNPNQYVEFTPTDDQITTPYIVVNGHIDPNSKGLALRSTLVGYNSNIIFRS	301
Dd		461	QVRISFNNAQYKVFEPFTDDQITTPYIVVNGHIDPASGTDLNRSTIFYGDSNFIFRS	520
Qy		302	MSMDNEVAFNNGGSGDGIDKRPVPEQPDE	331
Dd		521	MSMDNEVAFNNGGSGDGIDKRPVPEQPDE	550
RESULT		11		
ID	ABU16402		standard; protein; 935 AA.	
AC	ABU16402;			
XX				
XX	19-JUN-2003	(first entry)		
Dt				
XX				
Dd			Protein encoded by prokaryotic essential gene #1929.	
XX				
KX			Antisense; prokaryotic essential gene; cell proliferation; drug design.	
OS				
XX			Staphylococcus aureus.	
PN	MO200277183-A2.			
PD	03-OCT-2002.			
XX				
Pf	21-MAR-2002; 2002MCO-US009107.			
XX				
FR	21-MAR-2001; 2001US-00815242.			
PR	06-SEP-2001; 2001US-00948993.			
PR	25-OCT-2001; 2001US-0342923P.			
PR	08-FEB-2002; 2002US-00072851.			
PR	06-MAR-2002; 2002US-0362699P.			
XX				
FA	(ELIT-) ELITRA PHARM INC.			
XX				
Pi	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,			
Pi	Wall D, Trautick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH,			
DR	N-PSSDs; ACA20272.			
XX				
XX			New antisense nucleic acids, useful for identifying proteins or screening	
PT	for homologous nucleic acids required for cellular proliferation to			
PT	isolate candidate molecules for rational drug discovery programs.			
XX				
PS	Claim 25; SEQ ID NO 44326; 176bp; English.			
CC			The invention relates to an isolated nucleic acid comprising any one of	
CC			the 6213 antisense sequences given in the specification where expression	
CC			of the nucleic acid inhibits proliferation of a cell. Also included are:	
CC			(1) a vector comprising a promoter operably linked to the nucleic acid	
CC			encoding a polypeptide whose expression is inhibited by the antisense	
CC			nucleic acid; (2) a host cell containing the vector; (3) an isolated	
CC			polypeptide or its fragment whose expression is inhibited by the	
CC			antisense nucleic acid; (4) an antibody capable of specifically binding	
CC			the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular	

RESULT 13
 ADA89664
 ID ADA89664 standard; protein; 496 AA.
 XX
 AC ADA89664;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus antigenic protein #203.
 XX
 KM anti-genic protein; vaccine; Staphylococcus aureus; pathogenic organism;
 KM antibacterial; neuroprotective; immunosuppressive; anti-inflammatory;
 KM antitumor; immunostimulant; ophthalmological; pathogenic microbe;
 KM bacteraemia; septic shock; organ infection; skin infection;
 KM bacterial basal colonisation; bacterial eye infection; septicaemia;
 KM tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
 KM sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
 KM necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
 KM gastro-enteritis; dysentery; shigellosis; skin disorder.
 KM
 XX Staphylococcus aureus.
 OS
 XX
 PN MO2003011899-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 02-AUG-2002; 2002MO-GB003606.
 XX
 PR 02-AUG-2001; 2001GB-00018825.
 PR 09-JAN-2002; 2002GB-00000349.
 XX
 PA (UYSH-) UNIV SHEFFIELD.
 PA (BIOS-) BIOSYNEXUS INC.
 XX
 PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;
 XX
 DR WPI, 2003-256434/25.
 XX
 PT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
 PT useful as a vaccine for immunizing humans against e.g. bacteraemia, septic
 PT shock, septicaemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
 PT impetigo.
 XX
 PS Claim 4; Page 161; 189pp; English.
 CC
 CC The present invention describes an antigenic protein or its part, which
 CC is for use as a vaccine. The antigenic protein is encoded by an isolated
 CC DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
 CC sequences (designated dnaSA and dna SE, respectively) and which encodes a
 CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
 CC composition comprising at least one antigenic protein; (2) a method of
 CC immunising an animal against a disease or condition caused by a
 CC pathogenic microbe by administering the antigenic protein or the vaccine;
 CC (3) an antibody or its binding part obtainable by the method above; (4)
 CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 CC hybridoma cell line produced by the method of (4); and (6) identifying
 CC opsonic antigens expressed by a pathogenic microbe. The antigenic
 CC proteins have antibacterial, neuroprotective, immunosuppressive,
 CC anti-inflammatory, antitumor, immunostimulant and ophthalmological
 CC activities, and can be used in vaccines. The antigenic proteins or
 CC vaccines can be used for immunising an animal (specifically a human)
 CC against a disease or condition caused by a pathogenic microbe, e.g.
 CC bacteraemia, septic shock, organ infection, skin infection, bacterial
 CC basal colonisation, bacterial eye infections, septicaemia, tuberculosis,
 CC bacteria-associated food poisoning, blood infections, peritonitis,
 CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
 CC strep throat, streptococcal-associated toxic shock, necrotising
 CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
 CC dysentery, shigellosis, S. aureus-associated septicaemia, food-poisoning,
 CC skin disorders, S. epidermidis-associated septicaemia, peritonitis or
 CC endocarditis. The present sequence represents a S. aureus antigenic
 CC protein sequence from the present invention.

SQ Sequence 496 AA;
 Query Match 82.7%; Score 1433; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.1e-94;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 VAAADAPAGTDTNQLNLTAVGIDSGTTPVPHQAGYKLNKNGSVNSAVKGDTEKITV 61
 DB 221 VAAADAPAGTDTNQLNLTAVGIDSGTTPVPHQAGYKLNKNGSVNSAVKGDTEKITV 280
 OY 62 KEMLNNGVTSTAKPPTMAGDQVLANGVDSGNVYTFPDYNTQDVAKLTMTAYID 121
 DB 281 KEMLNNGVTSTAKPPTMAGDQVLANGVDSGNVYTFPDYNTQDVAKLTMTAYID 340
 OY 122 PENVKKTGNVTLATGISTTANKTVLDYKPKFYNLSIKGTIDQDKNTNTYRQTIYV 181
 DB 341 PENVKKTGNVTLATGISTTANKTVLDYKPKFYNLSIKGTIDQDKNTNTYRQTIYV 400
 OY 182 NPSGDNVIAPIVLTGNLKPNTDSNALIDQNTSIRKTVKVNAAULSESYPNPNFEDVTN 241
 DB 401 NPSGDNVIAPIVLTGNLKPNTDSNALIDQNTSIRKTVKVNAAULSESYPNPNFEDVTN 460
 OY 242 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHID 277
 DB 461 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHID 496
 RESULT 14
 ADA89663
 ID ADA89663 standard; protein; 496 AA.
 XX
 AC ADA89663;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Staphylococcus aureus antigenic protein #202.
 XX
 KM anti-genic protein; vaccine; Staphylococcus aureus; pathogenic organism;
 KM antibacterial; neuroprotective; immunosuppressive; anti-inflammatory;
 KM antitumor; immunostimulant; ophthalmological; pathogenic microbe;
 KM bacteraemia; septic shock; organ infection; skin infection;
 KM bacterial basal colonisation; bacterial eye infection; septicaemia;
 KM tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
 KM sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
 KM necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
 KM gastro-enteritis; dysentery; shigellosis; skin disorder.
 KM
 XX Staphylococcus aureus.
 OS
 XX
 PN MO2003011899-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 02-AUG-2002; 2002MO-GB003606.
 XX
 PR 02-AUG-2001; 2001GB-00018825.
 PR 09-JAN-2002; 2002GB-00000349.
 XX
 PA (UYSH-) UNIV SHEFFIELD.
 PA (BIOS-) BIOSYNEXUS INC.
 XX
 PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;
 XX
 DR WPI, 2003-256434/25.
 XX
 PT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
 PT useful as a vaccine for immunizing humans against e.g. bacteraemia, septic
 PT shock, septicaemia, tuberculosis, meningitis, pneumonia, gonorrhoea or
 PT impetigo.
 XX
 PS Claim 4; Page 160-161; 189pp; English.
 CC
 CC The present invention describes an antigenic protein or its part, which

CC is for use as a vaccine. The antigenic protein is encoded by an isolated
 CC DNA molecule of *Staphylococcus aureus* or *S. epidermidis* partial gene
 CC sequences (designated dSA and dSA SE, respectively); and which encodes a
 CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
 CC composition comprising at least one antigenic protein; (2) a method of
 CC immunising an animal against a disease or condition caused by a
 CC pathogenic microbe by administering the antigenic protein or the vaccine;
 CC (3) an antibody or its binding part obtainable by the method above; (4)
 CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
 CC hybridoma cell line produced by the method of (4); and (6) identifying
 CC opsonic antigens expressed by a pathogenic microbe. The antigenic
 CC proteins have antibacterial, neuroprotective, immunosuppressive,
 CC anti-infective, antitumor, immunostimulant and ophthalmological
 CC activities, and can be used in vaccines. The antigenic proteins or
 CC vaccines can be used for immunising an animal (specifically a human)
 CC against a disease or condition caused by a pathogenic microbe, e.g.
 CC bacteraemia, septic shock, organ infection, skin infection, bacterial
 CC basal colonisation, bacterial eye infections, septicaemia, tuberculosis,
 CC bacteria-associated food poisoning, blood infections, peritonitis,
 CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
 CC strep throat, streptococcal-associated toxic shock, necrotising
 CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
 CC dysentery, shigellosis, *S. aureus*-associated septicemia, food-poisoning,
 CC skin disorders, *S. epidermidis*-associated septicemia, peritonitis or
 CC endocarditis. The present sequence represents a *S. aureus* antigenic
 CC protein sequence from the present invention.

SQ Sequence 496 AA;

Query Match 82.7%; Score 1433; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.1e-94;
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGDITNOLNNTVNGIDSGTTPVPHQAGYKLVNGSVPSAVKSGPTFTVP 61
 DB 221 VAADAPAGDITNOLNNTVNGIDSGTTPVPHQAGYKLVNGSVPSAVKSGPTFTVP 280
 QY 62 KEMLNAGVTSTAKVPIIMAGDQVLAVNGIDSGNVIYTFDVTYNTKDVAKLTMPAYID 121
 DB 281 KEMLNAGVTSTAKVPIIMAGDQVLAVNGIDSGNVIYTFDVTYNTKDVAKLTMPAYID 340
 QY 122 PENVKATGNVTLAGIGSTTANKVTVVDEYKGFYMLSTKGTIDQDKTNMYRQITTY 181
 DB 341 PENVKATGNVTLAGIGSTTANKVTVVDEYKGFYMLSTKGTIDQDKTNMYRQITTY 400
 QY 182 NPSGDNTIAPVLTGNLKPNTDSNALIDQNTSIVKYKVDNAADLSESYFVNPENFEDVTN 241
 DB 401 NPSGDNTIAPVLTGNLKPNTDSNALIDQNTSIVKYKVDNAADLSESYFVNPENFEDVTN 460
 QY 242 SVNTTFPNPNOYKTEFNTPDQITTPYIVVNGHID 277
 DB 461 SVNTTFPNPNOYKTEFNTPDQITTPYIVVNGHID 496

RESULT 15

ABU15854

ID ABU15854 standard; protein, 961 AA.

AC ABU15854;

DT 19-JUN-2003 (first entry)

DE Protein encoded by prokaryotic essential gene #1381.

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS *Staphylococcus aureus*.

PN WO200277183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US0009107.

XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Wang J, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GT, Yamamoto R, Foreyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PEDB; ACA19724.

PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS Claim 25; SEQ ID NO 43778; 1766p; English.

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 623 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 961 AA;

Query Match 24.0%; Score 416.5; DB 6; Length 961;
 Best Local Similarity 29.1%; Pred. No. 2.9e-21;
 Matches 101; Conservative 69; Mismatches 144; Indels 33; Gaps 9;

QY 2 VAADAPAGDITNOLNNTVNGIDSGTTPVPHQAGYKLVNGSVPSAVKSGPTFTVP 57
 DB 158 VAADAPAGDITNOLNNTVNGIDSGTTPVPHQAGYKLVNGSVPSAVKSGPTFTVP 217
 QY 58 ITVPKELNAGVTSTAKVPIIMAGDQVLAVNGIDSGNVIYTFDVTYNTKDVAKLTMPAYID 115
 DB 218 ITVPKELNAGVTSTAKVPIIMAGDQVLAVNGIDSGNVIYTFDVTYNTKDVAKLTMPAYID 277
 QY 116 MPAYIDPENVKATGNVTLAGIGSTTANKVTVVDEYKGFYMLSTKGTIDQDKTNMYRQITTY 170
 DB 278 MPAYIDPENVKATGNVTLAGIGSTTANKVTVVDEYKGFYMLSTKGTIDQDKTNMYRQITTY 333
 QY 171 TNNYRQITTYNPSGDNTIAPVLTGNLKPNTDSNALIDQNTSIVKYKVDNAADLSESYF 230


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Db      334 EHGKSHFAYVKNNQSLSVTVTGOVTSQYKQSA----NNPTVKYKHIGSDELAESVY 389
QY      231 V--NPNEDVTNSVNITFENENQKVEFNTPDQITTPYIVVNGHIDPNSKGDALR 287
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Db      390 AKLDDTSKFEDVTEKVNLSYTSNGGYTLNLGDLDN--SKDYVIKYEGEYDQNAK-DLNR 446
QY      288 STLGYNSNIWR-----SMNDNEYAFNNSGSGGIDKXPVVP 326
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      447 THLSGHHKYPPYPPYPPVQLTWNGVAFYSNNAKGDGKDKPNDP 493

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Search completed: March 26, 2004, 05:03:55
 Job time : 130.592 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 05:00:12 ; Search time 34.6259 Seconds
(without alignments)
493.509 Million cell updates/sec

Title: US-10-056-052A-4
Perfect score: 1732
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum March 0%
Maximum March 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1732	100.0	345	3	US-08-856-253-7 Sequence 7, Appli
2	1727	99.7	933	3	US-08-293-728-2 Sequence 2, Appli
3	1727	99.7	933	3	US-09-421-868-2 Sequence 2, Appli
4	1723	99.5	936	4	US-08-956-171E-8249 Sequence 5249, Ap
5	353	20.4	930	4	US-09-134-001C-5314 Sequence 5314, Ap
6	353	20.4	930	4	US-09-386-962C-10 Sequence 10, Appli
7	331	19.1	1027	4	US-08-956-171E-5254 Sequence 5254, Ap
8	323.5	18.7	1166	4	US-09-200-650E-7 Sequence 7, Appli
9	312.5	18.0	918	4	US-09-200-650E-7 Sequence 7, Appli
10	282.5	16.3	251	4	US-08-956-171E-5252 Sequence 5252, Ap
11	257.5	14.9	1315	4	US-09-200-650E-5 Sequence 5, Appli
12	210.5	12.2	930	4	US-09-200-650E-3 Sequence 3, Appli
13	204	11.8	1112	2	US-08-714-402-2 Sequence 2, Appli
14	204	11.6	1161	4	US-09-327-536-2 Sequence 2, Appli
15	201.5	11.6	1742	4	US-09-386-962C-4 Sequence 4, Appli
16	139.5	8.1	358	4	US-09-134-000C-4597 Sequence 4597, Ap
17	136	7.9	559	4	US-08-956-171E-5251 Sequence 5251, Ap
18	131	7.6	2504	4	US-09-328-352-5821 Sequence 5821, Ap
19	129.5	7.5	1216	4	US-09-134-000C-5130 Sequence 5130, Ap
20	129.5	7.5	1391	4	US-10-080-505-11 Sequence 11, Appli
21	127.5	7.4	952	4	US-09-107-532A-4706 Sequence 4706, Ap
22	124.5	7.2	1391	4	US-10-080-505-15 Sequence 15, Appli
23	123.5	7.1	1411	4	US-10-080-505-17 Sequence 17, Appli
24	123	7.1	731	4	US-09-107-532A-6999 Sequence 6999, Ap
25	122.5	7.1	2385	4	US-09-543-681A-6304 Sequence 6304, Ap
26	121.5	7.0	992	4	US-09-206-942-61 Sequence 61, Appli
27	121.5	7.0	998	4	US-09-206-942-59 Sequence 59, Appli

28	120.5	7.0	920	4	US-09-463-402-6 Sequence 6, Appli
29	120.5	7.0	921	4	US-09-889-572-4 Sequence 4, Appli
30	120	6.9	737	4	US-09-071-035-460 Sequence 460, App
31	120	6.9	2032	4	US-09-071-035-458 Sequence 458, App
32	120	6.9	2032	4	US-09-071-035-462 Sequence 462, App
33	120	6.9	2032	4	US-09-071-035-466 Sequence 466, App
34	120	6.9	2054	4	US-09-134-000C-6612 Sequence 6612, Ap
35	118	6.8	789	4	US-09-002-285-94 Sequence 94, Appli
36	118	6.8	789	4	US-09-589-477-94 Sequence 65, Appli
37	117	6.8	1180	4	US-09-206-942-65 Sequence 63, Appli
38	117	6.8	1188	4	US-09-206-942-63 Sequence 96, Appli
39	116	6.7	789	4	US-09-002-285-96 Sequence 96, Appli
40	116	6.7	789	4	US-09-589-477-96 Sequence 96, Appli
41	116	6.7	3892	4	US-09-328-352-5503 Sequence 5503, Ap
42	115.5	6.7	405	4	US-09-328-352-5500 Sequence 5300, Ap
43	115.5	6.7	949	4	US-09-198-452A-478 Sequence 478, App
44	115	6.6	790	3	US-08-960-780-4 Sequence 4, Appli
45	115	6.6	790	3	US-09-073-898-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-856-253-7
Sequence 7, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Syranam, Narayana
APPLICANT: Syranam, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856/253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TANK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-7
Query Match 100.0%; Score 1732; ~DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAADAPAAAGTDTTNOITNTVTVGIDSGTIVYPHQAGVYKLANGFSPNSAVKGDTEKITVP 60
DB 13 MVAADAPAAAGTDTTNOITNTVTVGIDSGTIVYPHQAGVYKLANGFSPNSAVKGDTEKITVP 72
QY 61 PKELINGVSTAKVPPIAAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAVI 120
DB 73 PKELINGVSTAKVPPIAAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAVI 132
QY 121 DPENVKKTGNVTLATIGSTTANKTVLVDEKYGKFNLSIGTIDQIDKTNNTYRQITIV 180
DB 133 DPENVKKTGNVTLATIGSTTANKTVLVDEKYGKFNLSIGTIDQIDKTNNTYRQITIV 192
QY 181 VNPBGDGVIAFVLTGNLKPNTDSNALIDQNTSIRKYKVDNAADLSSEYFVNPENFEDVT 240
DB 193 VNPBGDGVIAFVLTGNLKPNTDSNALIDQNTSIRKYKVDNAADLSSEYFVNPENFEDVT 252
QY 241 NSVNTTTPNNQYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWR 300
DB 253 NSVNTTTPNNQYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWR 312
QY 301 MSMDNEVAFNNGSGGSDGIDKPVPEQDPE 331
DB 313 MSMDNEVAFNNGSGGSDGIDKPVPEQDPE 343

RESULT 2
US-08-293-728-2
Sequence 2, Application US/08293728D
Patent No. 6008341
GENERAL INFORMATION:
APPLICANT: Foster, Timothy J.
APPLICANT: McDevitt, Damien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: US/08/293,728D
CURRENT FILING DATE: 1994-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 933
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-293-728-2

Query Match 99.7%; Score 1727; DB 3; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.9e-141; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;

QY 2 VAADAPAAAGTDTTNOITNTVTVGIDSGTIVYPHQAGVYKLANGFSPNSAVKGDTEKITVP 61
DB 221 VAADAPAAAGTDTTNOITNTVTVGIDSGTIVYPHQAGVYKLANGFSPNSAVKGDTEKITVP 280
QY 62 KELINGVSTAKVPPIAAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAVI 121
DB 281 KELINGVSTAKVPPIAAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAVI 340
QY 122 PENVKKTGNVTLATIGSTTANKTVLVDEKYGKFNLSIGTIDQIDKTNNTYRQITIV 181
DB 341 PENVKKTGNVTLATIGSTTANKTVLVDEKYGKFNLSIGTIDQIDKTNNTYRQITIV 400
QY 182 NPSGDNVIAFVLTGNLKPNTDSNALIDQNTSIRKYKVDNAADLSSEYFVNPENFEDVTN 241
DB 401 NPSGDNVIAFVLTGNLKPNTDSNALIDQNTSIRKYKVDNAADLSSEYFVNPENFEDVTN 460
QY 242 SVNTTTPNNQYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWR 301
DB 461 SVNTTTPNNQYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWR 520
QY 302 MSMDNEVAFNNGSGGSDGIDKPVPEQDPE 331
DB 521 MSMDNEVAFNNGSGGSDGIDKPVPEQDPE 550

RESULT 3
US-09-421-868-2
Sequence 2, Application US/09421868
Patent No. 617084
GENERAL INFORMATION:
APPLICANT: Foster, Timothy J.
APPLICANT: McDevitt, Damien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: US/09/421,868
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 08/293,728
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 933
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-421-868-2

Query Match 99.7%; Score 1727; DB 3; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.9e-141; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;

QY 2 VAADAPAAAGTDTTNOITNTVTVGIDSGTIVYPHQAGVYKLANGFSPNSAVKGDTEKITVP 61
DB 221 VAADAPAAAGTDTTNOITNTVTVGIDSGTIVYPHQAGVYKLANGFSPNSAVKGDTEKITVP 280
QY 62 KELINGVSTAKVPPIAAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAVI 121
DB 281 KELINGVSTAKVPPIAAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAVI 340
QY 122 PENVKKTGNVTLATIGSTTANKTVLVDEKYGKFNLSIGTIDQIDKTNNTYRQITIV 181
DB 341 PENVKKTGNVTLATIGSTTANKTVLVDEKYGKFNLSIGTIDQIDKTNNTYRQITIV 400
QY 182 NPSGDNVIAFVLTGNLKPNTDSNALIDQNTSIRKYKVDNAADLSSEYFVNPENFEDVTN 241
DB 401 NPSGDNVIAFVLTGNLKPNTDSNALIDQNTSIRKYKVDNAADLSSEYFVNPENFEDVTN 460
QY 242 SVNTTTPNNQYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWR 301
DB 461 SVNTTTPNNQYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWR 520
QY 302 MSMDNEVAFNNGSGGSDGIDKPVPEQDPE 331
DB 521 MSMDNEVAFNNGSGGSDGIDKPVPEQDPE 550

RESULT 4
US-08-956-171E-5249
Sequence 5249, Application US/08956171E
Patent No. 6593118
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

Mon Mar 29 10:05:53 2004

us-10-056-052a-4.ra1

Page 3

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; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5249:
US-08-956-171E-5249
Query Match 99.5%; Score 1723; DB 4; Length 936;
Best Local Similarity 99.7%; Pred. No. 4,3e-141;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNOJTNVTGIDSGTIVYPHQAGYVKLNKGFSPNSAVKQDTFKITVP 61
DB 230 VAADAPAGTDTITNOJTNVTGIDSGTIVYPHQAGYVKLNKGFSPNSAVKQDTFKITVP 289
QY 62 KEININGVTSTAKVPIMAGDOVLANGVIDSDGNVITFTDVTNKKDKVATLTMPAYID 121
DB 290 KEININGVTSTAKVPIMAGDOVLANGVIDSDGNVITFTDVTNKKDKVATLTMPAYID 349
QY 122 PENVKKTGNVLTATIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIV 181
DB 350 PENVKKTGNVLTATIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIV 409
QY 182 NPSGDNVIAVLTGNKKNPTSDNALIDQONTSIKYKKVNADLSSESYVNVNENFEDVTN 241
DB 410 NPSGDNVIAVLTGNKKNPTSDNALIDQONTSIKYKKVNADLSSESYVNVNENFEDVTN 469
QY 242 SVNITPPNNOYKVEFNTDDQITTPYIVVANGHIDPNSKGLALRSTLYGNSNIWRS 301
DB 470 SVNITPPNNOYKVEFNTDDQITTPYIVVANGHIDPNSKGLALRSTLYGNSNIWRS 529
QY 302 MSWMDNEVAARNNGSGSDGIDKPVPEQDPE 331
DB 530 MSWMDNEVAARNNGSGSDGIDKPVPEQDPE 559

RESULT 5
US-09-134-001C-5314
; Sequence 5314, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: CTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
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; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5314
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5314
Query Match 20.4%; Score 353; DB 4; Length 930;
Best Local Similarity 30.6%; Pred. No. 4,7e-22;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLNVTGIDSGTIVYPHQAGYVKLNKGFSPNSAVKQDTFKITVPKEINLVGTS 71
DB 284 VTDQ--SITEGYDSDGIRKADENLIVTEVDKVSQDITVNIIDKNTVPSDLTD 341
QY 72 TAKVPIPMAGD-QVLANGVID-SDGNVITFTDYNTKODVKAATLTMPAYIDPENVKKTG 129
DB 342 SFAIPKIKDNGSEIILATGYDNTNKKQITFTFDVVKYENIKAHILKLTSIDSKVPNNN 401
QY 130 ---NVTLAGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIVNPSGD 186
DB 402 TKLDVEYKIALSS--VNKTIIVYQKPNENRANLQSMFTNIDTKNHTVEQITIVNPL-- 457
QY 187 NVIAPVLTGNLKPNTPSDNALIDQONTSIKYKKVNADLSSESYV-NPENFEDVTNSVNI 245
DB 458 RYSAKENNVNISGNGDEGSTIIDSTIIKYKKGDNQNLPSNRIRYDSEVEDVTNDVYA 517
QY 246 TFPNPNQYKVEFNTDDQITTPYIVVANGHIDPNSKGD-----LALRSTLYGNSNI 298
DB 518 QLGNNVDVNIIFG---NIDSPYIIKISKYDN-KDYTTIQQTVMQTTINEYIGE-- 570
QY 299 WRSWMDNEVAARNNGSGSDGIDKPVPEQ 328
DB 571 FRTASVNTIATFSTSSGQGG-DLP--PEK 597

RESULT 6
US-09-386-962C-10
; Sequence 10, Application US/09386962C
; Patent No. 6635473
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS
; FILE REFERENCE: P0635US2/BAS
; CURRENT APPLICATION NUMBER: US/09/386,962C
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-386-962C-10
Query Match 20.4%; Score 353; DB 4; Length 930;
Best Local Similarity 30.6%; Pred. No. 4,7e-22;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLNVTGIDSGTIVYPHQAGYVKLNKGFSPNSAVKQDTFKITVPKEINLVGTS 71
DB 284 VTDQ--SITEGYDSDGIRKADENLIVTEVDKVSQDITVNIIDKNTVPSDLTD 341
QY 72 TAKVPIPMAGD-QVLANGVID-SDGNVITFTDYNTKODVKAATLTMPAYIDPENVKKTG 129
DB 342 SFAIPKIKDNGSEIILATGYDNTNKKQITFTFDVVKYENIKAHILKLTSIDSKVPNNN 401
QY 130 ---NVTLAGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIVNPSGD 186
DB 402 TKLDVEYKIALSS--VNKTIIVYQKPNENRANLQSMFTNIDTKNHTVEQITIVNPL-- 457
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QY 187 NVIAPVLGNLKPNTDSNALIDQONTSIKYKYVDNAADLESYFV-NPENFEDVTNSVNI 245
DB 458 RLSAKETNNNISGNBEGSTIIDSTIIKYKYGVGNQNPDSNRIVDYSEYEDVTNDVYA 517
QY 246 TFPNPQKYVEFTPDQITTPYIVVNGHIDPNSKGD-----LALSTLYGNSNI 298
DB 518 QLGNNNDVINFG---NIDSPYIIKYISKYDPN-KDYTTTQQVTWQTTINEITGE-- 570
QY 299 WRSMWMDNEVAFNNGSGGDIKPVPEQ 328
DB 571 FRTASYDNTIAFSTSSGQGG-DLP--PEK 597

RESULT 7

US-08-956-171E-5254

Sequence 5254, Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Pannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: P848P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:

SEQUENCE CHARACTERISTICS:

LENGTH: 1027 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5254:

US-08-956-171E-5254

Query Match 19.1%; Score 331; DB 4; Length 1027;
Best Local Similarity 24.6%; Pred. No. 4.4e-20;
Matches 82; Conservative 77; Mismatches 146; Indels 28; Gaps 11;

QY 10 GTDINQJLNTVYDSC---TTPYFQAGVYKLVGFSVNSAVKGDFTKIVPKEIN 65
DB 203 GTDVSQVLT-VEIGSIEGHNNNTNKVEPAGRAVLKTKFENGHGQDFDFTLSNNV 261

QY 66 LINGTSTAKYPPIMAGDQVLANGVIDSDGNVITFTDYVNTKQDKATLTPAYIDPENY 125
DB 262 THGVSTARKVPEIKNGSVVVAATGEVLEGKIRTFETNDLEOKVDVTAELINLFIDPKIV 321
QY 126 KKTGNTLATIGSTTANKTVLVY-ERYGKFYNLSIKGTIDQIDXTNNYRQTIYVNS 184
DB 322 QTNNGQITITSLNEBQSKELDVYKKGIDIGNY-ANLNGSIEFPNKNRFSHVAIKEN 380
QY 185 GDNVIAVLGNLKPNTDSNALIDQONTSIKYKYVDNAADLESYFV-NPENFEDVT 240
DB 381 NGKTTSTVYVGTLMKGSNQG---NQPKRIFEYGNEDIKSVYANTTDSKREVT 436
QY 241 NSV-NITFPNPQKYVEFTPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNI 298
DB 437 SNMGNLNLQNGSYSUNI-----ENLDKTYVHYHDEY-LNGTDEVDFRTQVGHBEQVY 491
QY 299 -----WRSMWMDNEVAFNNGSGGDIKPVV 325
DB 492 KYYYDRGYTLTWMDGLVLYSKRANGNEKNGPII 524

RESULT 8

US-09-200-650E-7

Sequence 7, Application US/09200650E

Patent No. 6680195

GENERAL INFORMATION:

APPLICANT: Patti, Joseph M.

APPLICANT: Foster, Timothy J.

APPLICANT: Hook, Magnus A.O.

APPLICANT: Edihim, Samuel N.

APPLICANT: Perkins, Samuel L.

FILE REFERENCE: P06283US2/BAS

TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus

CURRENT APPLICATION NUMBER: US/09/200,650E

CURRENT FILING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: 60/066,815

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: 60/098,427

PRIOR FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 1166

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-200-650E-7

Query Match 18.7%; Score 323.5; DB 4; Length 1166;
Best Local Similarity 31.2%; Pred. No. 2.4e-19;
Matches 111; Conservative 53; Mismatches 137; Indels 55; Gaps 18;

QY 2 VAAAPAACTD.TNQTNTVT-----VGI DSGTIVPHQAGVYKLVGFSVNSAVKGDFT 56
DB 269 VQAPAAVSNV-NLILVTKQTIKVGKONVAAAHGKQIEVDTEFTDNKVKKGGITM 327
QY 57 KI-----TVPEKLNNGVSTAKVPPIMAGD---QVLANGVID-SDGNVITFTDYVNTK 107
DB 328 TINYDKNVIPSDL-----TDKNDPIITDPSGVIKGFEDKATKQIYTFEDYVYKY 380
QY 108 DVYKATLTPAYIDPENY-KKTGAVTLATIGSTTANKTVLVYERYKGFYNSIKGTI 165
DB 381 EDIKSRLLTYSYIDKKTVPNETSLMTFATGKETSN-Q-VVVDQDPMHGDSNISQIF 438
QY 166 DQIDKTNNTYRQTIYVNP---SGDNVIAVL-----TGNLKPNTDSNALIDQONTSIKY 216
DB 439 TKLDEBKQTIHQOIYVNPPLKSAITKVDIAGSQVDVGNILKNGS-TIID-QNTEIKV 496
QY 217 YKYVDNAADLESYFV-NPENFEDVTNSVNTTPNPQKYVEFTPD-DQITTPYIVVNG 274
DB 497 YKYNISQQLPQSNRIYDFSQYEDVTSQ---FDNKKFSNNVATLDFGIDNSAVYIIKYVS 552
QY 275 HIDPNSKGPL-----ALRST-LYGYNSNIIWRSMWMDNEVAFNNGSGGDIKPV 323

Db 553 KYPTSDGELDIAGQTSMTTDPKGY-----YNYAGSYNFVTSNDTGGDGTVPK 603

RESULT 9
US-09-200-650E-1
; Sequence 1, Application US/09200650E
; Patent No. 6680195
; GENERAL INFORMATION:
; APPLICANT: Patti, Joseph M.
; APPLICANT: Foster, Timothy J.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Perkins, Samuel L.
; APPLICANT: Bidkin, Delirde Ni
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
; FILE REFERENCE: P06283US2/BAS
; CURRENT APPLICATION NUMBER: US/09/200,650E
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,815
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/098,427
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-200-650E-1

Query Match 18.0%; Score 312.5; DB 4; Length 918;
Best Local Similarity 24.9%; Pred. No. 1.5e-18;
Matches 92; Conservative 69; Mismatches 132; Indels 77; Gaps 15;
QY 6 APPAGDTITNQLTNVTVGIDSGTYYPHQAGYKLNYSFVSPNSAVKDPFKITVPKEIN 65
Db 213 ADKAGTINVDKVTASNFKLEK-TTPDPSNGTFMANFTVTDKXSGDYF----- 262
QY 66 LNVGTSTAKPPTMADQVLANGVID-----SGNVI----- 97
Db 263 -----TAKLP-----DSLNGSDVDYSNSNMTPLADIKSTNGDVVAATYDILTXYT 311
QY 98 YFTFDVYNTKDVKATLTPAYIDPENVKKTGNVTLATIGSTTANKTVLVYER-----Y 153
Db 312 FVFTDYVNNKENINGOSLPLFTDRAKAPKSGTYDANINIADEMFKNKITVYSSPIAGI 371
QY 154 GKTYNLSIKETIQIDIKTN--NTYRQTIYNS-----GDNVIAFVLTGMLKPTDSNALI 207
Db 372 DKNGANISSQIIGVDPASGQNTYKQTVFVNPQKQVLAJNTWV--YTKGYQDKIESSGKY 429
QY 208 DOQNTSIVKVVNNAADLSESYFVNP--ENFEDVTSV--NITFPNPGQKVFENPPDQ 263
Db 430 SADDTKRIFEVNDTSLDSYADPNDSYLKEVTOQFKRIYYEHPNVAISIKFG-----D 485
QY 264 ITTPYIVVNGHIDPNSKGPLALRSTLYGN-----SNIIKRSMSWNEVAFNNGSGSGG 319
Db 486 ITTYVVLVEGHYDNTGKN--LKTQVLCENVDPVNTRDYSIFGMNNEVVRVYGGGSAUG 542
QY 320 IDKRVVPEOP 329
Db 543 -DSAVNPKP 551

RESULT 10
US-08-956-171E-5252
; Sequence 5252, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5252:
; US-08-956-171E-5252
Query Match 16.3%; Score 282.5; DB 4; Length 251;
Best Local Similarity 29.1%; Pred. No. 9e-17;
Matches 72; Conservative 46; Mismatches 92; Indels 37; Gaps 7;
QY 2 VAAADPAAGDTITNQLTNVTVGIDSGT-----TYYPHQAGYKLNYSFVSPNSAV 51
Db 17 VVEETKATGIDVTNK-----VEVEGESEIVGHKODTNVAPNNAERVTLKXMKKFGSGIK 71
QY 52 KQDTFKITVPKELNMGVSTAKVPPTMAGD-QVLANGVIDSDGNVYTFIDYVNTKDV 110
Db 72 AGDYEDFPLSDNVNTHGSLTKRVEIKSTDGQVMAIGELIGERKRVYTFEYVQEKDL 131
QY 111 KATLMPAYIDPENVKKTGNVTLATIGSTTANKTVLVYD-----EKYKRYNLSIKGTI 165
Db 132 TAEISLNLFTPTTVTQGNQNVVEKLGSETTVSKIFNIOYIGSVRDWG-----VTANGRI 187
QY 166 DQIDKNTNTRYQTIYVNSGDNVIAFVLTGNL-----KPNDSNALIDQNTSIVRYVDN 221
Db 188 DTLNKVDGKFSHPAYMKRNQSLSSVTVGQVTKGNKRGVA-----NPTVAVYKHIG 239
QY 222 AADLSES 228
Db 240 SDDLAEIS 246
RESULT 11
US-09-200-650E-5
; Sequence 5, Application US/09200650E
; Patent No. 6680195
; GENERAL INFORMATION:
; APPLICANT: Patti, Joseph M.
; APPLICANT: Foster, Timothy J.
; APPLICANT: Hook, Magnus A.O.

```

; APPLICANT: Eidiham, Delidre N1
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
; FILE REFERENCE: P06283US2/BAS
; CURRENT APPLICATION NUMBER: US/09/200,650E
; CURRENT FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: 60/066,815
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/098,427
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 1315
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-200-650E-5

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Query Match      14.9%; Score 257.5; DB 4; Length 1315;
Best Local Similarity 26.9%; Pred. No. 1.5e-13;
Matches 88; Conservative 51; Mismatches 157; Indels 31; Gaps 12;

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QY 13 ITNOLIVVTVIGISGTVYVPHQAGYVXLNYGFSVPSNAVKGDTFKITVPEKELNAGVT-- 70
DB 251 ITNVTTLTVVDADKNNKIVPAQ-DYLSKSGITVDKVGSDYFTIKYSDTVQVGLNPE 309
QY 71 -----STAKVPPIMAGQVLANGVISDDGNI-VTFPDYVNTKDDYKATLTMAYIDPEN 124
DB 310 DIKNIGIKDP--NNGEITATAHKHTANNLITTFDYVDFRFSVQMGINYSIYMDADT 366
QY 125 VKKTGN-VTLATIGSTTANKTVLVDEYKGFYNLSIKG---TIDQIDKTNN--YRQ 177
DB 367 IPVKNDVEFNVITGNTTKTKTANIQYPDYVMEKNSIGSAFETVSHVGNKENPGYKQ 426
QY 178 TIYVPSGDVIAVLGNLKPNTDSNAL-IDQNTSIRYKTKDNADLSSEYFVNPEN 235
DB 427 TIYVPSNSLTKNAKLVQAVSHSSYPNNIGQINDVDIDIKIYQVFKYTLNKGVDVATKE 486
QY 236 FEDVTNSV--NITFPNPQYVEFNPDPDQITTPYIVVNGHID-PNSKGLALRSTLYG 292
DB 487 LTVDTNQLKITYGDNNSAVIDGND-----SAYVVMNTKPKYNTSESPITLVQATLS 542
QY 293 YNSNIWRSMSWNEVAFNNGSGSGDG 319
DB 543 STGN--KSVSTGNALGFTNNQSGAG 566

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RESULT 12
US-09-200-650E-3
; Sequence 3, Application US/09200650E
; Patent No. 6680195
; GENERAL INFORMATION:
; APPLICANT: Patti, Joseph M.
; APPLICANT: Foster, Timothy J.
; APPLICANT: Hook, Magnus A O.
; APPLICANT: Eidiham, Delidre N1
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
; FILE REFERENCE: P06283US2/BAS
; CURRENT APPLICATION NUMBER: US/09/200,650E
; CURRENT FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: 60/066,815
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/098,427
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 3
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-200-650E-3

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Query Match      12.2%; Score 210.5; DB 4; Length 930;
Best Local Similarity 23.1%; Pred. No. 1.1e-09;
Matches 83; Conservative 57; Mismatches 136; Indels 83; Gaps 16;

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QY 6 APAAGTIDTNQL--TNTVVGIDSG-----TTPYVPHQAGYVXLNYGFSVPSNAVKGDT 55
DB 178 APOGCTVNNCKVHSHSNIDIALDKHVNQGTGKIEFMAFTSSDVKLKANYILIDSVEKGT 237
QY 56 FKITVPEELNNGVTSYAKVPPIM-AGDQVLANGVIDSDGN-VIYTFDYVNTKDDYKAT 113
DB 238 FTFKYGYFRPDSVRLPSQTONLTYNAQGNIIAKGIYDSTNTTPTTYTPTNVVDQYVNRGS 297
QY 114 LTMAYIDPEN--VKKG-----NTLATIGSTTANKTVLVDEYKGFYNLSIKGITDQI 168
DB 298 FEQVAFARKKATATDKRAYKMEVTL-----GNDIYSEIIVDYG-----HKKQPLISST 347
QY 169 DKINN--TYRQITVYVPSGDNVIAVLTGNL-----KPNTDSNALIDQNTSIRYKVD 220
DB 348 NYINNEDELNRMTAVVNPQKATYTKQTFVTLTGKKNPNA-----KNFKIYEVT 397
QY 221 NAADSESYFVNPENFEDVNTSVNITFPNPV-----QYKY-EFNTPDQ 263
DB 398 DQNGFVDSFTPDTSKLKQVTDQFDVYISNDKKTATVDMKQSTSNKQYIIQVAYPDNS 457
QY 264 ITTPYIVVNGHIDPNSKGLALRSTLYGYSNIIWRSMSWNEVAFNNGSGSGDGIDK 322
DB 458 STD-----NGKIDYTLDTD---KTKY-----SWSNSYSVNGSGSTANGDQK 495

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RESULT 13
US-08-714-402-2
; Sequence 2, Application US/08714402
; Patent No. 5910441
; GENERAL INFORMATION:
; APPLICANT: ROCHA, Claudia
; APPLICANT: FISCHETTI, Vincent A.
; TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS
; STREET: P O Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,402
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 016921-097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-714-402-2

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Query Match      11.8%; Score 204; DB 2; Length 1112;
Best Local Similarity 22.8%; Pred. No. 5.4e-09;

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Matches 86; Conservative 72; Mismatches 145; Indels 74; Gaps 18;
QY 8 AAGTDITN--QLTNVTGIDS--GTT-----VPHQAGYKLNKGFVSVPNSAV--K 52
DB 142 AGSKDVSSSLQLENPKMSVSKYKTEVSSGADAFRNHAAVFKMSFELKQKDKSETINP 201
QY 53 GDTFKITVPEKELNKGVTSTAKVPPIM--AGDQVLANGVIDSDGN--VIYFTFDYVNTKDD 109
DB 202 GDTFVQLDRRLNPKGISQ--DIPKTIYSANSPALIGKHAENHOLITTFDIDYAGLDK 259
QY 110 VKATLTMPAYIDPE-----NVKKT-----GNVTLATGIGSTANKTVLVDYE 151
DB 260 VOLSAELSLFLENKEVLENTSISNFKSTIGQGEITYKGTAVNLVNGESTKESNYITNGLS 319
QY 152 KYGKFPNLSIKGTDIDKTNNTYROTIIYVNSGDNVIAVLTGNL---KNTDSNALI 207
DB 320 NVG-----GSIESYNETGEFFWYVYVNPRTVI--PYATNMLMGFRARSTSDLE 369
QY 208 DQONTN-----IKVYKVDNAADLSSEYFVNPENF---EDVTSVNIITFPNNOYKVEFN 258
DB 370 NDANTSSELGEIQVEVEPEGELPSSYGVDVTKLRLRDTITAGLNGQMTKQRIIDFG 429
QY 259 TPDQDITTPYIVVNGHIDPNSKGLDALSTLYGNS-----NITRSMNDNEVAFN 311
DB 430 --NNIQKKAFLIKVTGKTDSGR-PLVQSNLASFRGASEYAAFTPVGQNVYFQNEIALS 486
QY 312 NGSGSGDG---IDKPVY 325
DB 487 PSKSGSGKSEFTKPSI 503

RESULT 14
US-09-327-536-2
Sequence 2, Application US/09327536
Patent No. 6355477
GENERAL INFORMATION:
APPLICANT: FISCHETTI, Vincent A.
APPLICANT: ROCHA, Claudia
TITLE OF INVENTION: FIBROECTIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A
FILE REFERENCE: 022927-008
CURRENT APPLICATION NUMBER: US/09/327,536
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: US 08/714,402
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1161
TYPE: PRT
ORGANISM: SFPBP gene
US-09-327-536-2

Query Match 11.8%; Score 204; DB 4; Length 1161;
Best Local Similarity 22.8%; Pred. No. 5,7e-09;
Matches 86; Conservative 72; Mismatches 145; Indels 74; Gaps 18;

QY 8 AAGTDITN--QLTNVTGIDS--GTT-----VPHQAGYKLNKGFVSVPNSAV--K 52
DB 142 AGSKDVSSSLQLENPKMSVSKYKTEVSSGADAFRNHAAVFKMSFELKQKDKSETINP 201
QY 53 GDTFKITVPEKELNKGVTSTAKVPPIM--AGDQVLANGVIDSDGN--VIYFTFDYVNTKDD 109
DB 202 GDTFVQLDRRLNPKGISQ--DIPKTIYSANSPALIGKHAENHOLITTFDIDYAGLDK 259
QY 110 VKATLTMPAYIDPE-----NVKKT-----GNVTLATGIGSTANKTVLVDYE 151
DB 260 VOLSAELSLFLENKEVLENTSISNFKSTIGQGEITYKGTAVNLVNGESTKESNYITNGLS 319
QY 152 KYGKFPNLSIKGTDIDKTNNTYROTIIYVNSGDNVIAVLTGNL---KNTDSNALI 207
DB 320 NVG-----GSIESYNETGEFFWYVYVNPRTVI--PYATNMLMGFRARSTSDLE 369

QY 208 DQONTN-----IKVYKVDNAADLSSEYFVNPENF---EDVTSVNIITFPNNOYKVEFN 258
DB 370 NDANTSSELGEIQVEVEPEGELPSSYGVDVTKLRLRDTITAGLNGQMTKQRIIDFG 429
QY 259 TPDQDITTPYIVVNGHIDPNSKGLDALSTLYGNS-----NITRSMNDNEVAFN 311
DB 430 --NNIQKKAFLIKVTGKTDSGR-PLVQSNLASFRGASEYAAFTPVGQNVYFQNEIALS 486
QY 312 NGSGSGDG---IDKPVY 325
DB 487 PSKSGSGKSEFTKPSI 503

RESULT 15
US-09-386-962C-4
Sequence 4, Application US/09386962C
Patent No. 6635473
GENERAL INFORMATION:
APPLICANT: FOSTER, Timothy
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS
FILE REFERENCE: P06335US2/BAS
CURRENT APPLICATION NUMBER: US/09/386,962C
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/096,443
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/117,119
PRIOR FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 1742
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-386-962C-4

Query Match 11.6%; Score 201.5; DB 4; Length 1742;
Best Local Similarity 21.8%; Pred. No. 1,7e-08;
Matches 79; Conservative 59; Mismatches 146; Indels 79; Gaps 15;

QY 1 VWAADAPAGTDITN--QLTNVTGID-----SGTIVPHQAGYKLNKGFVSVPNSAVK 53
DB 364 MSLAEPNSGKNVADKXKINTPILSNKSNHANNVWIPSNBOFLKANYELDDSIKEG 423
QY 54 DTFKITVPEKELNKGVTSTAKVPPIMAGD--QVLANGVIDSDGN--VIYFTFDYVNTKDDVK 111
DB 424 DTFKITVPEKELNKGVTSTAKVPPIMAGD--QVLANGVIDSDGN--VIYFTFDYVNTKDDVK 111
QY 112 ATLTPAYIDPEN--VKKTGNVTLATGIGSTANKTVLVDYEKYGKFPNLSIKGTDIDK 170
DB 484 GSPFLIATPKRETAIKONQVPMETVIANEVKKDPIVD--YONKDDNTTAAVANVDN 540
QY 171 TNNYTRQTIYVNSGDN-----VIAPVLTGNLKN-----DPSNLIQOQNTSIVYK 218
DB 541 VNNKNEVYVLYNQNQNPRAKYPSTVKNSEFIPGEKYYVEVDITNMAVDSFNDL--- 596
QY 219 VDNAAADLSSEYFVNPENFEDVTNS-----VNITF-----PNNNOYKVEFNTPDDQ 263
DB 597 -----NSNVKQDVTSGFAPKVSADGTRVIDINFARSWANGKY----- 633
QY 264 ITTPYIVVNGHIDPNSKGLDALSTLY--GYNSNIIMSMNDNEVAFNNGSGSDGI 320
DB 634 -----IVTQAVPRTGTVYTWLRTGNTTNDVYEGTK--STTVYANGSSTAQG-- 684
QY 321 DKP 323
DB 685 DNP 687

Search completed: March 26, 2004, 05:10:48
Job time: 78.6259 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 05:00:12 ; Search time 12.6578 Seconds
(without alignments)
493.509 Million cell updates/sec

Title: US-10-056-052a-20

Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSQTLTI.....YYGXDGFVYWGQGLTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	78.2	119	1	US-07-634-278-60 Sequence 60, Appl
2	506	78.2	119	1	US-08-477-128-60 Sequence 60, Appl
3	506	78.2	119	1	US-08-474-040-60 Sequence 60, Appl
4	506	78.2	119	1	US-08-487-200-60 Sequence 60, Appl
5	506	78.2	119	3	US-08-484-537-60 Sequence 60, Appl
6	506	78.2	138	1	US-07-634-278-33 Sequence 33, Appl
7	506	78.2	138	1	US-08-477-128-33 Sequence 33, Appl
8	506	78.2	138	1	US-08-474-040-33 Sequence 33, Appl
9	506	78.2	138	1	US-08-487-200-33 Sequence 33, Appl
10	506	78.2	138	3	US-08-484-537-33 Sequence 33, Appl
11	502	77.6	113	2	US-08-606-293-6 Sequence 6, Appl
12	494.5	76.4	117	2	US-08-621-751A-8 Sequence 8, Appl
13	492	76.0	119	2	US-08-752-844-16 Sequence 16, Appl
14	492	76.0	119	2	US-08-591-196-16 Sequence 16, Appl
15	492	76.0	119	4	US-09-293-533-16 Patent No. 5455030
16	491.5	76.0	242	6	5455030-15
17	487.5	75.3	120	2	US-08-652-558-8 Sequence 8, Appl
18	487.5	75.3	120	3	US-09-254-189-5 Sequence 5, Appl
19	487.5	75.3	239	2	US-08-860-174A-2 Sequence 2, Appl
20	487	75.3	113	2	US-08-606-293-2 Sequence 2, Appl
21	486.5	75.2	120	2	US-08-652-558-38 Sequence 38, Appl
22	486	75.1	222	2	US-08-190-199A-67 Sequence 67, Appl
23	486	75.1	235	2	US-08-190-199A-61 Sequence 61, Appl
24	481.5	74.4	137	2	US-08-621-751A-4 Sequence 4, Appl
25	479.5	74.1	120	3	US-08-652-558-7 Sequence 7, Appl
26	479.5	74.1	120	3	US-09-254-189-4 Sequence 4, Appl
27	475.5	73.5	241	4	US-09-554-765-13 Sequence 13, Appl

28	471.5	72.9	116	3	US-08-397-411-3 Sequence 3, Appl
29	471.5	72.9	121	3	US-08-881-037-67 Sequence 67, Appl
30	471.5	72.9	273	3	US-08-397-411-6 Sequence 6, Appl
31	471.5	72.9	446	3	US-08-397-411-7 Sequence 7, Appl
32	468	72.3	116	2	US-08-308-494A-21 Sequence 21, Appl
33	467	72.2	119	1	US-08-667-769A-15 Sequence 15, Appl
34	467	72.2	119	1	US-08-667-769A-62 Sequence 62, Appl
35	467	72.2	119	5	PCT-US95-17082A-15 Sequence 15, Appl
36	467	72.2	119	5	PCT-US95-17082A-62 Sequence 62, Appl
37	466.5	72.1	120	2	US-08-652-558-4 Sequence 4, Appl
38	466.5	72.1	120	2	US-08-652-558-5 Sequence 5, Appl
39	466.5	72.1	120	3	US-09-254-189-2 Sequence 2, Appl
40	466.5	72.1	140	3	US-08-943-136-4 Sequence 4, Appl
41	466.5	72.1	140	4	US-08-973-518-4 Sequence 4, Appl
42	465.5	71.9	239	6	5455030-13 Patent No. 5455030
43	464.5	71.8	120	2	US-08-652-558-6 Sequence 6, Appl
44	464.5	71.8	120	3	US-09-254-189-3 Sequence 3, Appl
45	463	71.6	119	1	US-08-467-420A-62 Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-60
Sequence 60, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COBOLINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
SERRET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single

Mon Mar 29 10:05:49 2004

us-10-056-052a-20.ra1

Page 2

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7,4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQKESGPGIVKPSQSLITCTISGFSLSRYSVHWVROPPGKLEMLGIMGGNTDYN 60
DB 1 QVQKESGPGIVKPSQSLITCTISGFSLSRYSVHWVROPPGKLEMLGIMGGNTDYN 60
QY 61 SALKSRISKDNKSNQVFLKNSLTADTAIVYCAKGEFFYYGDFVYMGQGLIVTS 120
DB 61 AAFISRLTISKDNKSNQVFFKVNSLQPADTAIYCARAGD--YNYDGFAYMGQGLIVTS 118
QY 121 S 121
DB 119 A 119

RESULT 2

US-08-477-728-60
Sequence 60, Application US/08477728
Patent No. 5583089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-477-728-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7,4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQKESGPGIVKPSQSLITCTISGFSLSRYSVHWVROPPGKLEMLGIMGGNTDYN 60
DB 1 QVQKESGPGIVKPSQSLITCTISGFSLSRYSVHWVROPPGKLEMLGIMGGNTDYN 60
QY 61 SALKSRISKDNKSNQVFLKNSLTADTAIVYCAKGEFFYYGDFVYMGQGLIVTS 120
DB 61 AAFISRLTISKDNKSNQVFFKVNSLQPADTAIYCARAGD--YNYDGFAYMGQGLIVTS 118
QY 121 S 121
DB 119 A 119

RESULT 3

US-08-474-040-60
Sequence 60, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas P.
APPLICANT: COELING, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-474-040-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7.4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGGLVYPFSGQTLSTICTTSGFSLRSYVHWVRQPPGKLEWLGIMTGGGNTDYN 60
DB 1 QVQLKESGPGGLVYPFSGQTLSTICTTSGFSLRSYVHWVRQPPGKLEWLGIMTGGGNTDYN 60
QY 61 SALKSRISISKDNSKNQVFLKNNSLTADTAVYYCARKEPFYGYDGFVYWGQTLTVTS 120
DB 61 AAFISRLTISKDNSKQVFFKYNLSLPADTAIYYCARAGD--YNYDGFAYWGQTLTVTS 118
QY 121 S 121
DB 119 A 119

RESULT 4
US-08-487-200-60

; Sequence 60, Application US/08487200

; Patent No. 5693762

; GENERAL INFORMATION:

; APPLICANT: QUEEN, Cary L.

; APPLICANT: CO. Man Sung

; APPLICANT: SCHNEIDER, William P.

; APPLICANT: LANDOLFI, Nicholas F.

; APPLICANT: COELING, Kathleen L.

; APPLICANT: SELICK, Harold E.

; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,200

; FILING DATE: 7-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/634,278

; FILING DATE: 19-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/590,274

; FILING DATE: 28-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/310,252

; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/290,975

; FILING DATE: 28-DEC-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-002610

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-487-200-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7.4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGGLVYPFSGQTLSTICTTSGFSLRSYVHWVRQPPGKLEWLGIMTGGGNTDYN 60
DB 1 QVQLKESGPGGLVYPFSGQTLSTICTTSGFSLRSYVHWVRQPPGKLEWLGIMTGGGNTDYN 60
QY 61 SALKSRISISKDNSKNQVFLKNNSLTADTAVYYCARKEPFYGYDGFVYWGQTLTVTS 120
DB 61 AAFISRLTISKDNSKQVFFKYNLSLPADTAIYYCARAGD--YNYDGFAYWGQTLTVTS 118
QY 121 S 121
DB 119 A 119

RESULT 5
US-08-484-537-60

; Sequence 60, Application US/08484537

; Patent No. 6180370

; GENERAL INFORMATION:

; APPLICANT: QUEEN, Cary L.

; APPLICANT: CO. Man Sung

; APPLICANT: SCHNEIDER, William P.

; APPLICANT: LANDOLFI, Nicholas F.

; APPLICANT: COELING, Kathleen L.

; APPLICANT: SELICK, Harold E.

; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Knourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,537

; FILING DATE: 7-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/634,278

; FILING DATE: 19-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/590,274

; FILING DATE: 28-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/310,252

; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/290,975

; FILING DATE: 28-DEC-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-002600

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-484-537-60

Query Match 78.2%; Score 506; DB 3; Length 119;
Best Local Similarity 75.2%; Pred. No. 7.4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGVLPSPQSTISITCTISGFSLSRYSVHWVRQPPGKGLWLGMIWGNTDYN 60
DB 1 QVQLKSGPGVLPSPQSLITCTVSGFSVTSGVHWIRQSPGKGLWLGMIWGNTDYN 60
QY 61 SALKSRISIKNSKQVFLKNSLPAADTAVYYCARKEFFYYGDFYWGQGLTVTVS 120
DB 61 AAFISRLTISKNSKQVFFKNSLQPADTAVYYCARAD--YNDGFAYWGQGLTVTVS 118
QY 121 S 121
DB 119 A 119

RESULT 6
US-07-634-278-33

Sequence 33, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-33

Query Match 78.2%; Score 506; DB 1; Length 138;
Best Local Similarity 75.2%; Pred. No. 8.8e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGVLPSPQSTISITCTISGFSLSRYSVHWVRQPPGKGLWLGMIWGNTDYN 60
DB 20 QVQLKSGPGVLPSPQSLITCTVSGFSVTSGVHWIRQSPGKGLWLGMIWGNTDYN 79
QY 61 SALKSRISIKNSKQVFLKNSLPAADTAVYYCARKEFFYYGDFYWGQGLTVTVS 120
DB 80 AAFISRLTISKNSKQVFFKNSLQPADTAVYYCARAD--YNDGFAYWGQGLTVTVS 137
QY 121 S 121
DB 138 A 138

RESULT 7
US-08-477-728-33

Sequence 33, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-33

Query Match 78.2%; Score 506; DB 1; Length 138;
Best Local Similarity 75.2%; Pred. No. 8.8e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVOLKESGPGLVKPSQTLSTCTTIGFSLRSYVHWVROPKGLIEMIGMIGGNTDYN 60
DB 20 QVOLKESGPGLVQPSQSLSITCTVSGFVSVYGVHWRSPKGLIEMIGVIMSGSSTDYN 79
QY 61 SALKSRSLISKDKNKQVFLKXNSLTADTAVYICARKGEFYIGDGFVYWGQGLTVVS 120
DB 80 AAFISRLTISKDKNKQVFFKXVNSLQPADTAIYCARAGD--YNYDGFAYWGQGLTVVS 137
QY 121 S 121
DB 138 A 138

RESULT 8

US-08-474-040-33
Sequence 33, Application US/08474040
Patent No. 5693761

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-474-040-33

Query Match 78.2%; Score 506; DB 1; Length 138;
Best Local Similarity 75.2%; Pred. No. 8.8e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVOLKESGPGLVKPSQTLSTCTTIGFSLRSYVHWVROPKGLIEMIGMIGGNTDYN 60
DB 20 QVOLKESGPGLVQPSQSLSITCTVSGFVSVYGVHWRSPKGLIEMIGVIMSGSSTDYN 79
QY 61 SALKSRSLISKDKNKQVFLKXNSLTADTAVYICARKGEFYIGDGFVYWGQGLTVVS 120
DB 80 AAFISRLTISKDKNKQVFFKXVNSLQPADTAIYCARAGD--YNYDGFAYWGQGLTVVS 137
QY 121 S 121
DB 138 A 138

RESULT 9

US-08-487-200-33
Sequence 33, Application US/08487200
Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-487-200-33

Query Match 78.2%; Score 506; DB 1; Length 138;
Best Local Similarity 75.2%; Pred. No. 8.8e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGGLVPSQSLITCTISGFSLSRYSVHWVRQPPKGLKLEWLGIMWGNDYDYN 60
 DB 20 QVQLKESGPGGLVPSQSLITCTISGFSVTSYGVHWIRQSPKGLKLEWLGIMWGNDYDYN 79
 QY 61 SALKSRLLSKSKNSKNQVFLKNSLTPADTAIVYCARKEGFYGYDGFVYWGQGLTVTVS 120
 DB 80 AAFISRLTISKNSKSKQVFFKVNSLQPADTAIVYCARAGD--YNYDGFAYWGQGLTVTVS 137
 QY 121 S 121
 DB 138 A 138

RESULT 10
 US-08-484-537-33
 ; Sequence 33, Application US/08484537
 ; Patent No. 6180370
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Gary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William F.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,537
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/634,278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 138 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-484-537-33

Query Match 78.2%; Score 506; DB 3; Length 138;
 Best Local Similarity 75.2%; Pred. No. 8,8e-44;
 Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

DB 20 QVQLKESGPGGLVPSQSLITCTISGFSVTSYGVHWIRQSPKGLKLEWLGIMWGNDYDYN 79
 QY 61 SALKSRLLSKSKNSKNQVFLKNSLTPADTAIVYCARKEGFYGYDGFVYWGQGLTVTVS 120
 DB 80 AAFISRLTISKNSKSKQVFFKVNSLQPADTAIVYCARAGD--YNYDGFAYWGQGLTVTVS 137
 QY 121 S 121
 DB 138 A 138

RESULT 11
 US-08-606-293-6
 ; Sequence 6, Application US/08606293
 ; Patent No. 5874082
 ; GENERAL INFORMATION:
 ; APPLICANT: de Boer, Mark
 ; TITLE OF INVENTION: Humanized Anti-CD40 Monoclonal Antibodies and
 ; TITLE OF INVENTION: Fragments Capable of Blocking B Cell Activation
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
 ; STREET: 4560 Horton Street, P.O. Box 8097
 ; CITY: Emeryville
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94662-8097

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/606,293
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/070,158
 FILING DATE: 28-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveriede, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 27527/33157
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2718
 TELEFAX: (510) 655-3542
 TELEX: n/a
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-606-293-6

Query Match 77.6%; Score 502; DB 2; Length 113;
 Best Local Similarity 81.0%; Pred. No. 1,8e-43;
 Matches 98; Conservative 7; Mismatches 8; Indels 8; Gaps 2;

RESULT 12

US-08-621-751A-8

Sequence 8, Application US/08621751A

Patent No. 5882644

GENERAL INFORMATION:

APPLICANT: Chang, Chung N.

APPLICANT: Landolfi, Nicholas F.

APPLICANT: Martin, Ulrich

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND

NUMBER OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 17

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,751A

FILING DATE: 22-MAR-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 32115200100

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141 MRSN FOERS SFO

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-621-751A-8

Query Match 76.4%; Score 494.5; DB 2; Length 137;
Best Local Similarity 76.9%; Pred. No. 1.3e-42;
Matches 93; Conservative 14; Mismatches 11; Indels 3; Gaps 1;

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DB 20 QVQLKESGPGLVPSQTLITCTISGFSLSRYSVHWVROPFGKGLWLMIMGGNTDYN 79
QY 61 SALKSRISISKNSKQVFLKNSLTADTAVYYCARK-GEFYGGDGVVWVGGLTVY 120
DB 80 SALKSRISISKNSKQVFLKNSLTADTAVYYCARTGTGTFD---YWGQGLTVY 136
QY 121 S 121
DB 137 S 137

RESULT 13

US-08-752-844-16

Sequence 16, Application US/08752844

Patent No. 5935821

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Poon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CURRENT APPLICATION DATA:

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-752-844-16

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Best Local Similarity 78.7%; Pred. No. 1.3e-42;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

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DB 1 QVQLKESGPGLVPSQTLITCTISGFSLSRYSVHWVROPFGKGLWLMIMGGNTDYN 60
QY 61 SALKSRISISKNSKQVFLKNSLTADTAVYYCARK-GEFYGGDGVVWVGGLTVY 119
DB 61 SALKSRISISKNSKQVFLKNSLTADTAVYYCARK-GEFYGGDGVVWVGGLTVY 117

RESULT 14

US-08-591-196-16

Sequence 16, Application US/08591196

Patent No. 5977316

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Poon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 57

CURRENT APPLICATION DATA:

CORRESPONDENCE ADDRESS:

Mon Mar 29 10:05:49 2004

us-10-056-052a-20.ra1

Page 8

APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schief, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-591-196-16

Query Match 76.0%; Score 492; DB 2; Length 119;
Best Local Similarity 78.7%; Pred. No. 1.9e-42;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 QVQLKESGPGELVAPRSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGIMGGNTDYN 60
DB 1 QVQLKESGPGELVAPRSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGIMGGNTDYN 60
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DB 61 SALKSRLLSISKDNKSKQVFLKMSLTQDTPARYCAREXXXXYYAMD--YWGQGSVTV 117
QY 120 SS 121
DB 118 SS 119

RESULT 15
US-09-293-533-16
Sequence 16, Application US/09293533
Patent No. 6509016
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Poon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schief, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-293-533-16

Query Match 76.0%; Score 492; DB 4; Length 119;
Best Local Similarity 78.7%; Pred. No. 1.9e-42;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 QVQLKESGPGELVAPRSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGIMGGNTDYN 60
DB 1 QVQLKESGPGELVAPRSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGIMGGNTDYN 60
QY 61 SALKSRLLSISKDNKNOVFLKMSLTADPAVYYCARK-GEFYGYDGFYWGQGLTVTV 119
DB 61 SALKSRLLSISKDNKSKQVFLKMSLTQDTPARYCAREXXXXYYAMD--YWGQGSVTV 117
QY 120 SS 121
DB 118 SS 119

Search completed: March 26, 2004, 05:11:57
Job time: 51.6578 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2004, 05:07:57 ; Search time 381.665 Seconds
(without alignments)
82.955 Million cell updates/sec

Title: US-10-056-052a-20

Perfect score: 647

Sequence: 1 QVQLKESGPGLVKPSQTLSTI.....YGYDGFVYWGQGLVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US6_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US6_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	100.0	121	US-10-056-052-20	Sequence 20, Appl
2	605	93.5	121	US-10-056-052-12	Sequence 12, Appl
3	538.5	83.2	118	US-10-056-052-16	Sequence 16, Appl
4	524.5	81.1	118	US-10-056-052-8	Sequence 8, Appl
5	506	78.2	119	US-10-389-417-19	Sequence 19, Appl
6	506	78.2	119	US-10-389-155-19	Sequence 19, Appl
7	506	78.2	118	US-10-389-417-46	Sequence 46, Appl
8	506	78.2	118	US-10-389-155-46	Sequence 46, Appl
9	493	76.2	121	US-09-842-776A-52	Sequence 52, Appl
10	493	76.2	121	US-10-207-655-252	Sequence 252, App
11	493	76.2	271	US-10-207-655-254	Sequence 254, App
12	493	76.2	556	US-10-207-655-268	Sequence 268, App
13	492	76.0	119	US-10-239-656-23	Sequence 23, Appl
14	492	76.0	119	US-10-153-401-16	Sequence 16, Appl
15	491.5	76.0	119	US-10-140-555-2	Sequence 2, Appl

16	487.5	75.3	116	US-10-169-251-108	Sequence 108, App
17	487	75.3	138	US-10-374-531-8	Sequence 8, Appl
18	487	75.3	138	US-10-374-531-13	Sequence 13, Appl
19	484.5	74.9	116	US-10-194-975-100	Sequence 100, App
20	476	73.6	119	US-10-232-187-2	Sequence 2, Appl
21	475.5	73.5	241	US-10-353-721-13	Sequence 13, Appl
22	474.5	73.3	139	US-08-779-784-37	Sequence 37, Appl
23	472.5	73.0	120	US-10-194-975-112	Sequence 112, App
24	471.5	72.9	116	US-10-435-239-3	Sequence 3, Appl
25	471.5	72.9	116	US-10-435-239-6	Sequence 6, Appl
26	471.5	72.9	273	US-10-059-261-61	Sequence 61, Appl
27	471.5	72.9	333	US-10-435-259-7	Sequence 7, Appl
28	471.5	72.9	446	US-10-418-836-38	Sequence 38, Appl
29	471.5	72.9	972	US-10-418-836-38	Sequence 39, Appl
30	469.5	72.6	120	US-10-239-656-43	Sequence 43, Appl
31	469.5	72.6	120	US-10-239-656-43	Sequence 43, Appl
32	469.5	72.6	510	US-10-239-656-48	Sequence 48, Appl
33	469.5	72.6	510	US-10-239-656-48	Sequence 49, Appl
34	469.5	72.5	253	US-10-239-656-63	Sequence 63, Appl
35	468.5	72.4	139	US-09-881-823-4	Sequence 4, Appl
36	468.5	72.4	250	US-10-194-975-110	Sequence 10, App
37	467	72.2	119	US-10-144-644-15	Sequence 15, Appl
38	467	72.2	119	US-10-144-644-62	Sequence 62, Appl
39	466.5	72.1	135	US-08-779-784-32	Sequence 32, Appl
40	466.5	72.1	140	US-09-007-093-4	Sequence 4, Appl
41	466.5	72.1	140	US-10-428-734-4	Sequence 4, Appl
42	465.5	71.9	135	US-10-010-729-68	Sequence 68, Appl
43	465	71.9	117	US-10-371-797-11	Sequence 11, Appl
44	464.5	71.8	122	US-10-207-655-360	Sequence 360, App
45	464.5	71.8	141	US-10-207-655-359	Sequence 359, App

ALIGNMENTS

RESULT 1
US-10-056-052-20
Sequence 20, Application US/10056052
Publication No. US20030098656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CIFA PROTEIN
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 121
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-20
Query Match 100.0%; Score 647; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 9e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLKESGPGLVKPSQTLSTIGTISGFSLSRYSVHWVRPPGKLEWIKITWGSGNTDYN 60
DB 1 QVQLKESGPGLVKPSQTLSTIGTISGFSLSRYSVHWVRPPGKLEWIKITWGSGNTDYN 60

Mon Mar 29 10:05:49 2004

us-10-056-052a-20.rapb

Page 2

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Db				
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RESULT 2
US-10-056-052-12
; Sequence 12, Application US/10056052
; Publication No. US2003009656A1
; GENERAL INFORMATION:
; APPLICANT: PATRI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PAIEL, Pitalksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; FILE REFERENCE: P070639504/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 121
; TYPE: prt
; ORGANISM: Staphylococcus aureus
US-10-056-052-12

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[illegible]

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RESULT 3
US-10-056-052-16
; Sequence 16, Application US/10056052
; Publication No. US20030099656A1
;
GENERAL INFORMATION:
;
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
;
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . .
;
FILE REFERENCE: P07069US04/EAS
;
CURRENT APPLICATION NUMBER: US/10/056,052
;
CURRENT FILING DATE: 2002-04-19
;
PRIOR APPLICATION NUMBER: 60/308,116
;
PRIOR FILING DATE: 2001-07-30
;
PRIOR APPLICATION NUMBER: 60/298,413

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? PRIOR FILING DATE: 2001-06-18
? PRIOR APPLICATION NUMBER: 60/274,511
? PRIOR FILING DATE: 2001-03-12
? PRIOR APPLICATION NUMBER: 60/264,072
? PRIOR FILING DATE: 2001-01-26
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 16
? LENGTH: 118
? TYPE: rrt
? ORGANISM: Staphylococcus aureus
? US-10-056-052-16

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Query Match	83.2%	Score 538.5	DB 14	Length 118
Best Local Similarity	84.3%	Pred. No. 3.7e-45		
Matches 102; Conservative		6; Mismatches 10; Indels 3; Gaps 1		

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QY      1 QVQLKESGPGVLVPSQSTLSTCTTISGFSLSYSVHWTRQPPGKGLMLTWGGNTVDN 60
Db      1 QVQLKESGPGVLVAPQSLSLSTCTVSGFSLSYSVHWTRQPPGKGLMLTWGGNTVDN 60
QY      61 SALKSLSTISKUNSKQVFLKNNLSLTADLVVYCAKGEFFYYDGDFVWGGGLTVTS 120
Db      61 SALKSLSTISKUNSKQVFLKNNLSLTDDTLMYYCATA---YGNNSFWAAYGGGLTVTS 117
QY      121 S 121
Db      118 A 118

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RESULT 4
US-10-056-052-8
; Sequence 8, Application US/10056052
; Publication No. US20030099656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: FATEL, Pritiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
FILE REFERENCE: P0706US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 118
TYPE:
ORANISM: Staphylococcus aureus
US-10-056-052-8

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Query Match	81.1%;	Score 524.5;	DB 14;	Length 118;
Best Local Similarity	81.8%;	Pred. No. 8.7e-44;		
Matches 99; Conservative	7;	Mismatches 12;	Indels 3;	Gaps 1

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Db	1	QVHLKEGPGGLVAPSGSLSTCTTCTVSGFSLSRNIHWRFQPRGKGLVGMGGGNDYN	60
		
QY	61	SALKSRLLSKDKNSKQVFLKNNSLTPADTAVYCARKEGFYGGVGVVGGGLTVTS	120
		
Db	61	SALKSRLLSKDKNSKQVFLKNNSLQTDITAVYCA---SAYGNSWEAVYGGGLTVTS	117
		
QY	121	S	121

Db 118 A 118

RESULT 5
US-10-389-417-19Sequence 19, Application US/10389417
Publication No. US20040049014A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coelling, Kathleen L.
Selick, Harold E.TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew LLP

CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,417

FILING DATE: 13-Mar-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0300

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-389-417-19

Query Match

Best Local Similarity 78.2%; Score 506; DB 12; Length 119;

Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVSPQSLITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGAGNTDYN 60

DB 1 QVQLKESGPGLVSPQSLITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGAGNTDYN 60

QY 61 SALKSLISKDKNQVFLKNSLTADTAIYYCAKGEFYIYGYGFFYNGGTLTVTS 120

Db 61 AAFISRLTISKDKNQVFPKNSLQPADTAIYYCARAGD--YNYDGFAYWGQGLTVTVS 118

QY 121 S 121

Db 119 A 119

RESULT 6
US-10-389-155-19Sequence 19, Application US/10389155
Publication No. US20030229208A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coelling, Kathleen L.
Selick, Harold E.TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew LLP

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,155

FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0300

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-389-155-19

Query Match

Best Local Similarity 78.2%; Score 506; DB 15; Length 119;

Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVSPQSLITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGAGNTDYN 60

DB 1 QVQLKESGPGLVSPQSLITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGAGNTDYN 60

Mon Mar 29 10:05:49 2004

us-10-056-052a-20.rapb

Page 4

QY 61 SALKSLISKDNKQVFLKNSLTADTAVYCCARKGEFFYGVGDTLVTVS 120
DB 61 AAFISRLTISKDNKSKQVFFKYNLSLPADTAIYCCARAGD--YNYDGFAYWGOGTLTVTS 118
QY 121 S 121
DB 119 A 119

RESULT 7
US-10-389-417-46

Sequence 46, Application US/10389417
Publication No. US20040049014A1
GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung
Schneider, William P.
Landolfi, Nicholas P.
Coeligh, Kathleen L.
Selick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3634

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-Mar-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-10-389-417-46

Query Match 78.2%; Score 506; DB 12; Length 138;
Best Local Similarity 75.2%; Pred. No. 6,7e-42;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQSLTICTVSGFSLRYSVHWVQPPGKLEWLGIMGGNTDYN 60

DB 20 QVQLKESGPGLVKPSQSLTICTVSGFSLRYSVHWVQPPGKLEWLGIMGGNTDYN 79
QY 61 SALKSLISKDNKQVFLKNSLTADTAVYCCARKGEFFYGVGDTLVTVS 120
DB 80 AAFISRLTISKDNKSKQVFFKYNLSLPADTAIYCCARAGD--YNYDGFAYWGOGTLTVTS 137
QY 121 S 121
DB 138 A 138

RESULT 8
US-10-389-155-46

Sequence 46, Application US/10389155
Publication No. US20030229208A1
GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung
Schneider, William P.
Landolfi, Nicholas P.
Coeligh, Kathleen L.
Selick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3634

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-10-389-155-46

Query Match 78.2%; Score 506; DB 15; Length 138;
Best Local Similarity 75.2%; Pred. No. 6,7e-42;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQSLTICTVSGFSLRYSVHWVQPPGKLEWLGIMGGNTDYN 60

Db 20 QVQLKESGPGLVAPSGQSLITCTVSGFSLRSYVHWVROPKGLGEMLGIMGGANTDYN 79
QY 61 SALKSRSLISKDNKSNQVFLKNNSLTADTAVYYCARKEFFYYGDFVYWGQGLTVTS 120
Db 80 AAFISRLTISKDNKSKQVFFKVNSLQPDATLARYCARAGD--INVDGFAIYWGQGLTVTS 137
QY 121 S 121
Db 138 A 138

RESULT 9
US-09-842-776A-52
; Sequence 52, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-842-776A-52

Query Match 76.7%; Score 496; DB 12; Length 121;
Best Local Similarity 79.7%; Pred. No. 5,6e-41;
Matches 98; Conservative 8; Mismatches 13; Indels 4; Gaps 3;
QY 1 QVQLKESGPGLVAPSGQSLITCTVSGFSLRSYVHWVROPKGLGEMLGIMGGANTDYN 59
Db 1 EQVLESGPGLVAPSGQSLITCTVSGFSLRSYVHWVROPKGLGEMLGIMGGSTDY 60
QY 60 NSALKSRSLISKDNKSNQVFLKNNSLTADTAVYYCAR-GEFFYYGDFVYWGQGLTVT 118
Db 61 NSALKSRSLISKDNKSNQVFLKNNSLQTDPTAIFYCARMMGGGRYPDY--FDYWGQGLTVT 118
QY 119 VSS 121
Db 119 VSS 121

RESULT 10
US-10-207-655-252
; Sequence 252, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 252
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-252

Query Match 76.2%; Score 493; DB 14; Length 121;
Best Local Similarity 78.5%; Pred. No. 1.1e-40;

Matches 95; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 QVQLKESGPGLVAPSGQSLITCTVSGFSLRSYVHWVROPKGLGEMLGIMGGANTDYN 60
Db 1 EQVLESGPGLVAPSGQSLITCTVSGFSLRGYVHWVROPKGLGEMLGIMGGSTDYN 60
QY 61 SALKSRSLISKDNKSNQVFLKNNSLTADTAVYYCARKEFFYYGDFVYWGQGLTVTS 120
Db 61 SALKSRSLITKDNKSKQVFLKNNSLQTDPTAIFYCARDSYSNFHYVMDYWGQGSVTVS 120
QY 121 S 121
Db 121 S 121

RESULT 11
US-10-207-655-254
; Sequence 254, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 254
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-254

Query Match 76.2%; Score 493; DB 14; Length 271;
Best Local Similarity 78.5%; Pred. No. 2.7e-40;
Matches 95; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 QVQLKESGPGLVAPSGQSLITCTVSGFSLRSYVHWVROPKGLGEMLGIMGGANTDYN 60
Db 151 EQVLESGPGLVAPSGQSLITCTVSGFSLRGYVHWVROPKGLGEMLGIMGGSTDYN 210
QY 61 SALKSRSLISKDNKSNQVFLKNNSLTADTAVYYCARKEFFYYGDFVYWGQGLTVTS 120
Db 211 SALKSRSLITKDNKSKQVFLKNNSLQTDPTAIFYCARDSYSNFHYVMDYWGQGSVTVS 270
QY 121 S 121
Db 271 S 271

RESULT 12
US-10-207-655-268
; Sequence 268, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 268
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-268

Query Match 76.2%; Score 492; DB 14; Length 556;
 Best Local Similarity 78.5%; Pred. No. 5.9e-40;
 Matches 95; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVOLKESGPGVLVPSQTLISITCTISGFSLSRYSVHWVRQPPGKGLWLMIGGNTDYN 60
 DB 151 QVOLKESGGLVAPSSQSLITCTVSGFSLTGYVHWVRQPPGKGLWLMIGGNTDYN 210
 QY 61 SALKSRSLISKDNRKQVFLKNSLTADTAVYYCARKEGFYGYDGFYVWGQGLTVTVS 120
 DB 211 SALKSRSLISKDNRKQVFLKNSLTADTAVYYCARKEGFYGYDGFYVWGQGLTVTVS 270
 QY 121 S 121
 DB 271 S 271

RESULT 13

US-10-239-656-23
 ; Sequence 23, Application US/10239656
 ; Publication No. US20040038339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUTER, PETER
 ; APPLICANT: RIETHMULLER, GERT
 ; APPLICANT: LOTTERBUSE, RALF
 ; APPLICANT: BORSCHERT, KATRIN
 ; APPLICANT: KISCHEL, ROMAN
 ; APPLICANT: MAYER, MONIKA
 ; APPLICANT: HOMERSTER, ROBERT
 ; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
 ; TITLE OF INVENTION: TO AN EPITOPE OF THE NKGD2 RECEPTOR COMPLEX
 ; FILE REFERENCE: 029976/0106
 ; CURRENT APPLICATION NUMBER: US/10/239,656
 ; PRIOR FILING DATE: 2003-03-06
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03414
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: EP 00106467.4
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKGD2
 ; OTHER INFORMATION: hybridoma 6H7E7 variable heavy chain
 ; US-10-239-656-23

Query Match 76.0%; Score 492; DB 12; Length 119;
 Best Local Similarity 77.7%; Pred. No. 1.3e-40;
 Matches 94; Conservative 10; Mismatches 15; Indels 2; Gaps 1;

QY 1 QVOLKESGPGVLVPSQTLISITCTISGFSLSRYSVHWVRQPPGKGLWLMIGGNTDYN 60
 DB 1 QVOLKESGPGVLVAPSSQSLITCTVSGFSLTGYVHWVRQPPGKGLWLMIGGNTDYN 60
 QY 61 SALKSRSLISKDNRKQVFLKNSLTADTAVYYCARKEGFYGYDGFYVWGQGLTVTVS 120
 DB 61 SALKSRSLISKDNRKQVFLKNSLTADTAVYYCARKEGFYGYDGFYVWGQGLTVTVS 118
 QY 121 S 121
 DB 119 S 119

RESULT 14
 US-10-153-401-16
 ; Sequence 16, Application US/10153401
 ; Publication No. US20030114398A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chatterjee, Malaya

Foon, Kenneth A.
 Chatterjee, Sunil K.
 TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
 TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/153,401
 FILING DATE: 27-Aug-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/293,533
 FILING DATE: 1999-04-15
 APPLICATION NUMBER: US 08/372,676
 FILING DATE: 1995-01-17
 APPLICATION NUMBER: US 08/591,196
 FILING DATE: 1996-01-16

ATTORNEY/AGENT INFORMATION:
 NAME: Catherine M. Polizzi
 REGISTRATION NUMBER: 40,130
 REFERENCE/DOCKET NUMBER: 304142000202
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-10-153-401-16

Query Match 76.0%; Score 492; DB 14; Length 119;
 Best Local Similarity 78.7%; Pred. No. 1.3e-40;
 Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 QVOLKESGPGVLVPSQTLISITCTISGFSLSRYSVHWVRQPPGKGLWLMIGGNTDYN 60
 DB 1 QVOLKESGGLVAPSSQSLITCTVSGFSLTGYVHWVRQPPGKGLWLMIGGNTDYN 60
 QY 61 SALKSRSLISKDNRKQVFLKNSLTADTAVYYCAR-GEFYGYDGFYVWGQGLTVTVS 119
 DB 61 SALKSRSLISKDNRKQVFLKNSLTADTAVYYCARXXXXXXXXXXIYAMD---YWGQGLTVTVS 117
 QY 120 SS 121
 DB 118 SS 119

RESULT 15
 US-10-140-555-2
 ; Sequence 2, Application US/10140555
 ; Publication No. US20020127227A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Julie A. Abrahamson
 ; APPLICANT: Stephen D. Holmes
 ; APPLICANT: Jeffrey R. Jackson
 ; TITLE OF INVENTION: RHAMM Antagonist Antibodies
 ; FILE REFERENCE: P50857

; CURRENT APPLICATION NUMBER: US/10/140,555
 ; CURRENT FILING DATE: 2002-05-07
 ; PRIOR APPLICATION NUMBER: US/09/443,790
 ; PRIOR FILING DATE: 1999-11-19
 ; PRIOR APPLICATION NUMBER: 60/109,041
 ; PRIOR FILING DATE: 1998-11-19
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-140-555-2

Query Match 76.0%; Score 491.5; DB 13; Length 119;
 Best Local Similarity 79.3%; Pred. No. 1.5e-40;
 Matches 96; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY	1	QVQLKESGPGELVPSQTLSTITCTISGFSLSRYSVHWVROPCKGLEWLGIMWGNTDYN	60
Db	1	QVQLKESGPGELVAPSOISITCTVSGFSLTGYGVNWRQPGKLEWLGIMWVGSTDYN	60
QY	61	SALKSRISIKDNSKNOVFLKNSLTADTAVVYCARKEFFYYGYDGFVYWGQGLVTVS	120
Db	61	SALKSRISIKDNSKNOVFLKNSLTQTDPTARYCARGGSSLL--GFAYWGQGLVTVS	117
QY	121	S 121	
Db	118	A 118	

Search completed: March 26, 2004, 05:54:12
 Job time : 409.665 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:17 ; Search time 12.4433 Seconds
(without alignments)
935.380 Million cell updates/sec

Title: US-10-056-052A-20

Perfect score: 647
Sequence: 1 QVQKESGPGLVKPSQTLST.....YGYDFVWVGQGLTVTSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	534.5	82.6	117	2	S38563 Ig heavy chain V r
2	489	75.6	114	2	S11106 Ig heavy chain V r
3	489	75.6	140	2	S55028 Ig heavy chain V r
4	488	75.4	127	2	B31807 Ig heavy chain V r
5	487.5	75.3	122	2	S20809 Ig heavy chain V r
6	486.5	75.2	139	2	A32456 Ig heavy chain pre
7	482.5	74.6	122	2	A49049 Ig heavy chain V r
8	482	74.5	144	1	G2WS14 Ig heavy chain pre
9	478.5	74.0	135	2	S31913 Ig gamma-2A chain
10	477	73.7	112	2	S11100 Ig heavy chain V r
11	477	73.7	113	2	S11101 Ig heavy chain V r
12	476.5	73.6	115	2	S26470 Ig heavy chain V r
13	472	73.0	116	2	S11102 Ig heavy chain V r
14	470	72.6	140	2	S14238 Ig gamma-1 chain p
15	466.5	72.1	116	2	S42484 Ig heavy chain V r
16	465.5	71.9	141	2	S52446 Ig heavy chain V r
17	465.5	71.9	144	2	S11244 Ig gamma-2a chain
18	465	71.9	121	2	D30087 Ig heavy chain V r
19	464.5	71.8	120	2	P10087 Ig heavy chain V r
20	464	71.7	114	2	S11099 Ig heavy chain V r
21	463	71.6	111	2	S26324 Ig heavy chain V r
22	459	70.9	115	2	S11103 Ig heavy chain V r
23	457.5	70.7	118	2	S32786 Ig heavy chain (an
24	457	70.6	115	2	S11107 Ig heavy chain V r
25	452	69.9	110	2	S26323 Ig heavy chain V r
26	452	69.9	118	2	P00266 Ig heavy chain V r
27	451	69.7	112	2	S11108 Ig heavy chain V r
28	450	69.6	231	2	PC4155 Ig gamma-2b chain
29	448.5	69.3	107	2	S14492 Ig heavy chain V r

30	447.5	69.2	107	2	S14493 Ig heavy chain V r
31	447	69.1	106	2	S26322 Ig heavy chain V r
32	443	68.5	109	2	PH1026 Ig heavy chain V r
33	443	68.5	112	2	S11098 Ig heavy chain V r
34	441.5	68.2	107	2	S14491 Ig heavy chain V r
35	441.5	68.2	110	2	PH1024 Ig heavy chain V r
36	440	68.0	121	2	S33131 Ig heavy chain V r
37	439.5	67.9	106	2	S14489 Ig heavy chain V r
38	437	67.5	117	2	S10111 Ig heavy chain pre
39	435	67.2	116	2	PH1098 anti-DNA autoantib
40	434	67.1	115	2	PHMS14 Ig heavy chain pre
41	433	66.9	109	1	PH1025 Ig heavy chain V r
42	433	66.9	114	2	S26321 Ig heavy chain V r
43	433	66.9	114	2	S11104 Ig heavy chain V r
44	431.5	66.7	107	2	S14506 Ig heavy chain V r
45	428	66.2	114	2	S11105 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S38563
Ig heavy chain V region (ASM61) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S38563
R/Monester, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.

A/Description: Molecular analysis of mercury-induced anti-nuclear antibodies in H-2s M

A/Reference number: S38559

A/Accession: S38563

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-117 <MON>

A/Cross-references: EMBL:X75099; NID:G414151; PIDN:CAA52990.1; PID:G414152

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 534.5; DB 2; Length 117;
Best Local Similarity 85.0%; Pred. No. 9e-43;
Matches 102; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY	1	QVQKESGPGLVKPSQTLSTCTISGFSRSVSHVWVROPGRGLMIGMGNTDYN	60
DB	1	QVQKESGPGLVKPSQTLSTCTISGFSRSVSHVWVROPGRGLMIGMGNTDYN	60
QY	61	SALKSRSLISKDMSKNQVFLKMSLTADTAVVYCARKEGFYGYDGFVWVGQGLTVTS	120
DB	61	SALKSRSLISKDMSKNQVFLKMSLTADTAVVYCARKEGFYGYDGFVWVGQGLTVTS	117

RESULT 2

S11106
Ig heavy chain V region (clone NOS-96.2) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000

[illegible]

RESULT 3
S55028
Ig heavy chain V region - mouse (fragment)
C|Species: Mus musculus (house mouse)
C|Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C|Accession: S55028
R|Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolis, M.N.; Sheriff,
J.M. Biol. 248, 344-360, 1995
A|Title: Structure and specificity of the anti-disoxin antibody 40-50.
A|Reference number: S55027; PMID:95257394; PMID:7739045
A|Accession: S55028
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-140 <DEF>
A|Cross-References: EMBL:L31403; NID:ig476717; PIDN:AAA38191.1; PID:ig476718
C|Superfamily: Immunoglobulin V region; Immunoglobulin homology
C|Keywords: heteroc tetramer; immunoglobulin
E|34-116/Domain: immunoglobulin homology <IMM>

Query Match	75.6%;	Score 489;	DB 2;	Length 140;
Best Local Similarity	77.8%;	Pred. No.1.8e-38;		
Matches	95;	Conservative	8;	Mismatches 17; Indels 2; Gaps 2;
QY	1 QVQLKESGGLVSPQTLSITCTISGFSLSRYSVHWRCPPGKGLEWLGIMWGSGNTDYN	60		
Db	20 QVHLKESGGIVAPSSGLSITCTVSQGSFLTTGVHMFRCPPGKGLELGIIMAGSNTDYN	75		
QY	61 SALKRSLISKDNKKQVFINKNSLTADTAVYYCAR-KGEFYYIGDEGYIWGGCLITY	119		
Db	80 SALMSRLSTINKDNKSQGVFIKNSSLADDDPTAMYYCARFRPASYDY-AVDYWGGISTVT	138		
QY	120 SS 121			
Db	139 SS 140			

RESULT 4
B31807
Ig heavy chain V region (PAC1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 23-May-1997
C:Accession: B31807
R:Tab: R.; Gould, R.J.; Garzky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt
U: Biol. Chem. 264, 250-255, 1989
A:Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequ
A:Reference number: A31807; PMID:89079661; PMID:2905518
A:Accession: B31807
A:Status: preliminary
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-127 <TAU>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IM>

```

Query Match      75.4%; Score 488; DB 2; Length 127;
Best Local Similarity 72.4%; Pred. No. 2,1e-38;
Matches 92; Conservative 11; Mismatches 18; Indels 6; Gaps 1;

```

Db I QVQLKSGSGGLVQPSSQSLTCTVSGSFELTSGYNHWRLSKGLKLEWLGIVIMSGGSIDYN 60
QY 61 SALKSLSTISKDNKNQVFLKKNSLTAADTAVYCAVKGFEYGYDQ-----FVWVSGG 114
Db 61 AATISRTSKISKDNKSQVFFKNMSLDANDTGLVTCARNSPSTYIYDQAGPIYANDYWGQG 120
QY 115 TLVTVSS 121
Db 121 TSVTVSS 127

RESULT 5
 S20809
 I:heavy chain V region (hybridoma C8) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S20809
 R:Hoggenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.
 submitted to the EMBL Data Library, September 1990
 A:Description: Nucleotide sequences of the variable region cDNAs encoding a murine anti-
 A:Reference number: S20809
 A:Accession: S20809
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-122 <HOO>
 A:Cross-References: EMBL:XS4692; NID:g50249; PIDN:CA38508.1; PID:g50250
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterocetamer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

	Query Match	75.3%	Score 487.5	DB 2:	Length 122;
	Best Local Similarity	75.8%	Pred. No. 2.2e-38;		
	Matches	94;	Conservative 10;	Mismatches 13;	Indels 7; Gaps 2
QY	2	VQLKESGPGVLRPSQTLSICTSGFSLSRYSVHWVRQPPGKLEMLGMINGGGNTDYN	61		
Dd	2	VPLVESGPGLVARSQSLSICTCTGSGFSLLGYGNWVRQPPGKLEMLGMINWDGSTDYN	61		
QY	62	ALKSRILISKDNKSNQVFLMNSLTADDAIVYYCAK---GEFYFGYDGFPYWGQCLV	11		
Dd	62	ALKRSLSTKDNSKSQFLKNLSLQTDTPARYYCAREFSYGNLIYYGMD---YWQGQSTV	11		
QY	118	TVSS 121			
Dd	119	TVSS 122			

RESULT 6
A32456
Ig heavy chain precursor V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Oct-1989 #sequence_rev:10 31-Dec-1993 #text_change 23-Jul-1999
C:Accession: A32456
R:Komdink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.M.
U:Bio. Chem.264, 4513-4522, 1989
A:Title: Variable region primary structures of a high affinity anti-fluorescein immunoglobulin
A:Reference number: A32456; M01D:89174706; PMID:2494173
A:Accession: A32456
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <DOM>
A:Cross-references: GB:004609; NID:G556316; PIDN:AAA50298.1; PID:G556317
A:Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue 3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match	75.2%	Score 486.5;	DB 2;	Length 139;
Best Local Similarity	77.0%	Pred. No. 3.4e-38;		
Matches 94;	Conservative 9;	Mismatches 14;	Indels 5;	Gaps

QY 2 VQAKSGGGLYKPSQTLITCTTIGGFLSKSYTHNRQPPGKLEMLGIMGGGNDVNS 61

Db 21 VLKESGPGVLVAPSGSLITCTVSGFSLTNGVHWVRQPPGKGLWGLVIMAGNTDYN 80
Qy 62 ALKSRSLISKDNKQVFLKQNSLTADTAIVYCARKEG--FYGYDGFVWGGTLTV 119
Db 81 ALMSLTLISKDNKSGVFLKQNSLTQDDTAIYCAKRLERIFYAMD--YWGQSTVTV 137
Qy 120 SS 121
Db 138 SS 139

RESULT 7
A49049
Ig heavy chain V region (anti-idiotypic) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C/Accession: A49049
R/Armstrong, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A/Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen
A/Reference number: A49049; MUID:93049629; PMID:1425914
A/Accession: A49049
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-122 <ARM>
A/Experimental source: BALB/c
A/Note: sequence extracted from NCBI backbone (NCBI:118295, NCBI:118296)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 482.5; DB 2; Length 122;
Best Local Similarity 76.0%; Pred. No. 6.4e-38;
Matches 92; Conservative 11; Mismatches 15; Indels 3; Gaps 1;
Qy 1 QVQLKESGPGVLVPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWGLVIMAGNTDYN 60
Db 1 QVQLKESGPGVLVAPSGSLITCTVSGFSLTNGVHWVRQPPGKGLWGLVIMAGNTDYN 60
Qy 61 SALKSRSLISKDNKQVFLKQNSLTADTAIVYCARKEGFYGYDGFVWGGTLTVS 120
Db 61 SALKSRSLISKDNKSGVFLKQNSLTQDDTAIYCAKRLERIFYAMD--YWGQSTVTVS 117
Qy 121 S 121
Db 118 S 118

RESULT 8
G2MS14
Ig heavy chain precursor V region (MOPC 141) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 16-Jun-2000
C/Accession: A02094
R/Sakano, H.; Maki, R.; Kurosawa, Y.; Roeder, W.; Tonggawa, S.
Nature 286, 676-683, 1980
A/Title: Two types of somatic recombination are necessary for the generation of complete
A/Reference number: A93229; MUID:81012133; PMID:6774258
A/Accession: A02094
A/Molecule type: DNA
A/Residues: 1-144 <SKK>
A/Cross-references: GB:V00768; GB:J00491; NID:951615; PIDN:CAA24149.1; PID:951616
A/Note: the sequence shown was determined from a differentiated gene isolated from a myeloma cell line. The authors translated the codon TAT for residue 51 as Thr and TTA for residue 9
C/Genetics: 16/1
A/Intons: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-97/Domain: immunoglobulin homology <IMM>
F/20-144/Product: Ig heavy chain V region (MOPC 141) #status predicted <MAT>
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 482; DB 1; Length 144;

Best Local Similarity 74.4%; Pred. No. 8.5e-38;
Matches 93; Conservative 9; Mismatches 19; Indels 4; Gaps 1;
Qy 1 QVQLKESGPGVLVPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWGLVIMAGNTDYN 60
Db 20 QVQLKESGPGVLVAPSGSLITCTVSGFSLTNGVHWVRQPPGKGLWGLVIMAGNTDYN 79
Qy 61 SALKSRSLISKDNKQVFLKQNSLTADTAIVYCARKEGFYGYDGFVWGGTLTVS 116
Db 80 STLKSRLLTLKDNKSGVFLKQNSLTQDDTAIYCAKSVSIYYGRDCKFTLDYWGQSTV 139
Qy 117 VTYS 121
Db 140 VTYS 144

RESULT 9
S31913
Ig gamma-2A chain precursor - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999
C/Accession: S31913
R/Bespalov, I.A.; Hiyaroy, P.A.; Lukashovich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponova,
submitted to the EMBL Data Library, January 1993
A/Reference number: S31913
A/Accession: S31913
A/Molecule type: mRNA
A/Residues: 1-135 <BB8>
A/Cross-references: EMBL:X70822; NID:957921; PIDN:CAA50153.1; PID:957922
A/Experimental source: strain BALB/c
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-11/Domain: signal sequence #status predicted <SIG>
F/12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 478.5; DB 2; Length 135;
Best Local Similarity 74.4%; Pred. No. 1.7e-37;
Matches 90; Conservative 13; Mismatches 13; Indels 5; Gaps 1;
Qy 1 QVQLKESGPGVLVPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWGLVIMAGNTDYN 60
Db 20 QVQLKESGPGVLVQSGSLITCTVSGFSLTNGVHWVRQPPGKGLWGLVIMAGNTDYN 79
Qy 61 SALKSRSLISKDNKQVFLKQNSLTADTAIVYCARKEGFYGYDGFVWGGTLTVS 120
Db 61 SALKSRSLISKDNKSGVFLKQNSLTQDDTAIYCAKRLERIFYAMD--YWGQSTVTVS 134
Qy 121 S 121
Db 135 S 135

RESULT 10
S11100
Ig heavy chain V region (clone NQ2-20.5.3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C/Accession: S11100
R/Karttunen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone
A/Reference number: S07331; MUID:83271467; PMID:6877353
A/Accession: S11100
A/Molecule type: mRNA
A/Residues: 1-112 <NMT>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 477; DB 2; Length 112;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
Matches 92; Conservative 8; Mismatches 12; Indels 8; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTICTTISGFSLSRYSVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
Db 1 QVQLKESGPGVLVPSQSLSITCTVSGSLTSGVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
QY 61 SALKSRSLISKDQKQVFLKQNSLTADTAIVYCARKEFFYYGDFVYWGQGLTVTS 120
|||
Db 61 SALKSRSLISKDQKQVFLKQNSLTQDDTAIVYCAR-----DRGYWGGQGLTVTS 112

RESULT 11
S11101
Ig heavy chain V region (clone NQ2-48.2.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C/Accession: S11101
R/Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone
A/Reference number: S07331; MUID:83271467; PMID:6877353
F/15-97/Domain: immunoglobulin homology <IMM>
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-113 <KAA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 477; DB 2; Length 113;
Best Local Similarity 76.0%; Pred. No. 1.9e-37;
Matches 92; Conservative 9; Mismatches 12; Indels 8; Gaps 1;
QY 1 QVQLKESGPGLVKPSQTLSTICTTISGFSLSRYSVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
Db 1 QVQLKESGPGVLVPSQSLSITCTVSGSLTSGVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
QY 61 SALKSRSLISKDQKQVFLKQNSLTADTAIVYCARKEFFYYGDFVYWGQGLTVTS 120
|||
Db 61 SALKSRSLISKDQKQVFLKQNSLTQDDTAIVYCAR-----DRGYWGGQGLTVTS 112
QY 121 S 121
Db 113 A 113

RESULT 12
S26470
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S26470
R/Kavaler, J.
submitted to the EMBL Data Library, April 1991
A/Reference number: S26459
A/Accession: S26470
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-115 <KAV>
A/Cross-references: EMBL:X59109; NID:951948; PIDN:CAA41835.1; PID:951949
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterocretamer; immunoglobulin
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 476.5; DB 2; Length 115;
Best Local Similarity 76.9%; Pred. No. 2.2e-37;
Matches 90; Conservative 10; Mismatches 14; Indels 3; Gaps 2;
QY 1 QVQLKESGPGLVKPSQTLSTICTTISGFSLSRYSVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
Db 1 QVQLKESGPGVLVPSQSLSITCTVSGFSLTSGVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
QY 61 SALKSRSLISKDQKQVFLKQNSLTADTAIVYCARKEFFYYGDFVYWGQGLTVTS 116
|||
Db 61 AAFISLISLISKDQKQVFLKQNSLTQDDTAIVYCARKN--YYGSSXWFAVWGQGLTVTS 115

RESULT 13
S11102
Ig heavy chain V region (clone NQ5-4.3.1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C/Accession: S11102
R/Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone
A/Reference number: S07331; MUID:83271467; PMID:6877353
F/15-97/Domain: immunoglobulin homology <IMM>
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-116 <NAT>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 472; DB 2; Length 116;
Best Local Similarity 75.2%; Pred. No. 5.8e-37;
Matches 91; Conservative 9; Mismatches 13; Indels 8; Gaps 1;
QY 1 QVQLKESGPGLVKPSQTLSTICTTISGFSLSRYSVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
Db 1 QVQLKESGPGVLVPSQSLSITCTVSGSLTSGVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
QY 61 SALKSRSLISKDQKQVFLKQNSLTADTAIVYCARKEFFYYGDFVYWGQGLTVTS 120
|||
Db 61 SALKSRSLISKDQKQVFLKQNSLTQDDTAIVYCAR-----DRGYWGGQGLTVTS 112
QY 121 S 121
Db 113 A 113

RESULT 14
S14238
Ig gamma-1 chain precursor (15CS) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S14238
R/Vandamme, A.M.; Bulens, F.; Bernat, H.; Nelles, L.; Lijnen, R.H.; Collier, D.
Eur. J. Biochem. 192, 767-775, 1990
A/Title: Construction and characterization of a recombinant murine monoclonal antibody di
A/Reference number: S14236; MUID:91006173; PMID:2209622
A/Accession: S14238
A/Molecule type: mRNA
A/Residues: 1-140 <VAN>
A/Cross-references: EMBL:X56392; NID:951619; PIDN:CAA39803.1; PID:9747853
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/26-108/Domain: immunoglobulin homology <IMM>

Query Match 72.6%; Score 470; DB 2; Length 140;
Best Local Similarity 73.6%; Pred. No. 1.1e-36;
Matches 89; Conservative 13; Mismatches 15; Indels 4; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTICTTISGFSLSRYSVHWVRQPPGKGLFWLGMVGGNTDYN 60
|||
Db 12 QVQLKESGPGVLVPSQSLSITCTVSGFSLTSGVHWVRQPPGKGLFWLGMVGGNTDYN 71
|||
QY 61 SALKSRSLISKDQKQVFLKQNSLTADTAIVYCARKEFFYYGDFVYWGQGLTVTS 120
|||
Db 72 AAFISLISLISKDQKQVFLKQNSLTQDDTAIVYCARN---YWG-TSDYWGQGLTVTS 127

QY 121 S 121
Db 128 S 128
RESULT 15
S42484
Ig heavy chain V region (4B1 VH) - mouse
C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
 C/Accession: S42484
 R/Gilbert, D.; Brard, F.; Margartite, C.; Delpech, A.; Tron, F.
 submitted to the EMBL Data Library, March 1994
 A/Description: An idiotype D3-bearing polypeptide, murine anti-DNA monoclonal antibody
 A/Reference number: S42484
 A/Accession: S42484
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-116 <GIL>
 A/Cross-references: EMBL:Z30962; NID:G461325; PIDN:CAA83216.1; PID:G461326
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 466.5; DB 2; Length 116;
 Best Local Similarity 72.7%; Pred. No. 1.9e-36;
 Matches 88; Conservative 13; Mismatches 15; Indels 5; Gaps 1;
 QY 1 QVQLKESGPGELVYPKSQTLSITTTISGFSISRYSVHWVROPQPKGLEMLGIMINGGNTDYN 60
 Db 1 QVQLQESGPGELVAPSGSLSTITCTVSGFSLTSVALISWVROPQPKGLEMLGVIMTGGGNTYN 60
 QY 61 SALKSRLLSISKDNSSKNQVFLKXNSLTADTAVTYCARKGSEFYGYDGFYWGQGLTVYS 120
 Db 61 SALKSRLLSISKDNSSKQIFKLNLSLOTDDARYFCARD-----GYSPFDYWGQGLTVYS 115
 QY 121 S 121
 Db 116 S 116

Search completed: March 26, 2004, 05:08:56
 Job time: 12.4433 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:51:26 ; Search time 7.29433 Seconds

(without alignments)
863.752 Million cell updates/sec

Title: US-10-056-052a-20

Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSQTLSI.....YYGYDGFVYWGQGLTVVSS 121

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	482	74.5	144	1 HV43_MOUSE
2	434	67.1	115	1 HV44_MOUSE
3	423	65.4	116	1 HV45_MOUSE
4	396.5	61.3	135	1 HV02_XENLA
5	374.5	57.9	122	1 HV3G_HUMAN
6	370.5	57.3	146	1 HV2I_HUMAN
7	365	56.4	137	1 HV46_MOUSE
8	349.5	54.0	122	1 HV3H_HUMAN
9	349	53.9	121	1 HV3J_HUMAN
10	346	53.5	117	1 HV2G_HUMAN
11	344	53.2	136	1 HV01_XENLA
12	342	52.9	119	1 HV2C_HUMAN
13	338.5	52.3	116	1 HV6I_MOUSE
14	338	52.2	129	1 HV2F_HUMAN
15	335.5	51.9	126	1 HV3K_HUMAN
16	333	51.5	113	1 HV47_MOUSE
17	333	51.4	119	1 HV3I_HUMAN
18	332.5	51.4	119	1 HV40_MOUSE
19	329.5	50.9	136	1 HV16_MOUSE
20	328.5	50.8	119	1 HV3J_MOUSE
21	325.5	50.3	114	1 HV3B_HUMAN
22	325.5	50.3	126	1 HV2A_HUMAN
23	324.5	50.2	119	1 HV38_MOUSE
24	322	49.8	118	1 HV39_MOUSE
25	322	49.8	142	1 HV01_RAT
26	318.5	49.2	116	1 HV6O_MOUSE
27	317.5	48.9	120	1 HV2B_HUMAN
28	316.5	48.9	116	1 HV3T_HUMAN
29	316	48.8	115	1 HV3D_HUMAN
30	316	48.8	123	1 HV25_MOUSE
31	314.5	48.6	122	1 HV3A_HUMAN
32	314	48.5	117	1 HV17_MOUSE
33	312	48.2	125	1 HV2D_HUMAN

ALIGNMENTS

RESULT 1	HV43_MOUSE	STANDARD	PRT	144 AA
34	311	48.1	116	1 HV05_CARAU
35	310.5	48.0	120	1 HV3U_HUMAN
36	310	47.9	119	1 HV3L_HUMAN
37	309	47.8	115	1 HV2J_MOUSE
38	308.5	47.7	114	1 HV2A_RABIT
39	308	47.6	117	1 HV62_MOUSE
40	308	47.6	120	1 HV3E_HUMAN
41	307.5	47.5	139	1 HV07_MOUSE
42	305	47.1	117	1 HV2B_RABIT
43	304	47.0	113	1 HV3O_MOUSE
44	303.5	46.9	122	1 HV2O_MOUSE
45	303.5	46.9	136	1 HV2C_RABIT

34	311	48.1	116	1 HV05_CARAU	P01861 carassius a
35	310.5	48.0	120	1 HV3U_HUMAN	P01782 homo sapien
36	310	47.9	119	1 HV3L_HUMAN	P01773 homo sapien
37	309	47.8	115	1 HV2J_MOUSE	P01801 mus musculu
38	308.5	47.7	114	1 HV2A_RABIT	P01827 oryctolagus
39	308	47.6	117	1 HV62_MOUSE	P18533 mus musculu
40	308	47.6	120	1 HV3E_HUMAN	P01766 homo sapien
41	307.5	47.5	139	1 HV07_MOUSE	P01751 mus musculu
42	305	47.1	117	1 HV2B_RABIT	P01828 oryctolagus
43	304	47.0	113	1 HV3O_MOUSE	P01799 mus musculu
44	303.5	46.9	122	1 HV2O_MOUSE	P01789 mus musculu
45	303.5	46.9	136	1 HV2C_RABIT	P01829 oryctolagus

Query Match 74.5% Score 482; DB 1; Length 144;
Best Local Similarity 74.4% Pred. No. 3.9e-43;
Matches 93; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

Qy	1	QVQLKESGPGLVKPSQTLSITCTIGSFLSRYSVMVWVQPPKGLKLTWTKMTGGNTDYN 60
Db	20	QVQLKESGPGLVKPSQTLSITCTIGSFLSRYSVMVWVQPPKGLKLTWTKMTGGNTDYN 79
Qy	61	SAKSLSTLSKNSKNQVFLKXNSLTADTAAYVCARGGEFYVG---YDGFVYWGQGLT 116

DB 80 STLSRLITKDNKSKQVFLKNNLSLQTDPTARYCASVSIIYYGRSDKYFTLDYMGQGT 139

QY 117 VTWSS 121
DB 140 VTWSS 144

RESULT 2

HV44_MOUSE STANDARD; PRT; 115 AA.

AC P01820; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Ig heavy chain V region P014 precursor.
OC Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;

RT "The nucleotide sequences of rearranged and germline immunoglobulin

of complete immunoglobulin heavy-chain genes."

RT Nature 286:676-683(1980).

CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.

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or send an email to license@sib-sib.ch).

CC EMBL: V00767; CAA24148.1; -

DR PIR: A02095; HVMS14.

DR PDB: 1A7N; 29-APR-98.

DR PDB: 1A7O; 29-APR-98.

DR PDB: 1A7P; 29-APR-98.

DR PDB: 1A7R; 29-APR-98.

DR PDB: 1G7H; 17-JAN-01.

DR PDB: 1G7I; 17-JAN-01.

DR PDB: 1G7J; 17-JAN-01.

DR PDB: 1G7M; 17-JAN-01.

DR PDB: 43C9; 24-JUL-02.

DR PDB: 43CA; 24-JUL-02.

DR InterPro: IPR007110; 1G-1-like.

DR InterPro: IPR003596; 1G_V.

DR Pfam: PF00047; 1G; 1.

DR SMART: SM00406; 1G; 1.

DR PROSITE: PS50835; 1G-Like; 1.

DR Immunoglobulin V region; Signal; 3D-structure.

DR SIGNAL 1 19

FT CHAIN 20 115 IG HEAVY CHAIN V REGION P014.

RESULT 3

HV45_MOUSE STANDARD; PRT; 116 AA.

AC P01821; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Ig heavy chain V region MC101 precursor.
OC Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;

RT "The nucleotide sequences of rearranged and germline immunoglobulin
of a mouse myeloma MC101 and evolution of VH genes in
mouse."

RT J. Biol. Chem. 257:277-285(1982).

CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.

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or send an email to license@sib-sib.ch).

CC EMBL: J00502; AAA38515.1; -

DR PIR: A02096; GMS10.

DR HSSP: P01772; 2F84.

DR InterPro: IPR007110; 1G-1-like.

DR InterPro: IPR003596; 1G_V.

DR Pfam: PF00047; 1G; 1.

DR SMART: SM00406; 1G; 1.

DR PROSITE: PS50835; 1G-Like; 1.

DR Immunoglobulin V region; Signal.

DR SIGNAL 1 19

FT CHAIN 20 116 IG HEAVY CHAIN V REGION MC101.

FT DOMAIN 20 >116 IG-LIKE.

FT NON_TER 116 116

FT SEQUENCE 116 AA; 12593 MW; 8079A6EB7C552B3E CRC64;

Query Match 65.4%; Score 423; DB 1; Length 116;

Best Local Similarity 79.4%; Pred. No. 4, 1e-37;

Matches 77; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLKESGPGGLVPSQITSLTCTISGFSLSRSYVHWQVQPKGLGLWLGIMGGNTDYN 60

DB 20 QVQLKESGPGGLVPSQISITCTVSGFSLTSYGVMWVQSPKGLGLWLGIMGGSDTDYN 79

RX MEDLINE=88176921; PubMed=2451244;
RA Schwaiger U., Mikoyak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RT Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J03632; AAA49791.1; -.
DR PIR; B31933; B31933.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region; Signal.
KW NON TER 1
FT SIGNAL 1
FT CHAIN 19 135
FT DOMAIN 20 128
FT NON_TER 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;
Query Match 61.3%; Score 396.5; DB 1; Length 135;
Best Local Similarity 61.0%; Pred. No. 2.8e-34;
Matches 72; Conservative 23; Mismatches 20; Indels 3; Gaps 2;
QY 4 LKSGPGGLVPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMIWGAGNTDYN 63
DB 21 LQSGPGGLVPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMIWGAGNTDYN 80
QY 64 KSRLSISKDQSKQVFLKQNSLTADTAAYVYCARKEPFYVYDGFFYWGQGLTVTV 121
DB 81 KNRVTLTKDQSKQVYLVQNGMEVKDTPAYYCAR--EYASGVN-FDYWGQGLTVTVTS 135
RESULT 5
ID HV3G HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RT Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02051; M3HUM.
DR HSSP; P01772; 2FBA.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region; Pyrolydione carboxylic acid.
KW DOMAIN 1 112
FT MOD_RES 1 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
Query Match 57.9%; Score 374.5; DB 1; Length 122;
Best Local Similarity 55.7%; Pred. No. 4.8e-32;
Matches 68; Conservative 24; Mismatches 29; Indels 1; Gaps 1;
QY 1 QVQLKESGPGGLVPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMI-WGAGNTDY 59
DB 1 QVELVESGGGVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKLEWVAIVSGBBKKY 60
QY 60 NSALKSRISISKDQSKQVFLKQNSLTADTAAYVYCARKEPFYVYDGFFYWGQGLTVTV 119
DB 61 ABSYKGRFTISRDSKSTLYLVQNSLRARETAYVYCARDRPLVGYRAFYWGQGLTVTV 120
QY 120 SS 121
DB 121 SS 122
RESULT 6
ID HV2I HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RT Gene 33:181-189 (1985).
DR PIR; A02101; G1H0B2.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146
FT DOMAIN 20 117
FT DOMAIN 118 127
FT DOMAIN 128 146
FT DISULFID 42 115
FT NON_TER 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FDS2BB218171F CRC64;
Query Match 57.3%; Score 370.5; DB 1; Length 146;
Best Local Similarity 58.1%; Pred. No. 1.5e-31;
Matches 75; Conservative 20; Mismatches 23; Indels 11; Gaps 3;
QY 1 QVQLKESGPGGLVPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMIWGAGNTDYN 60
DB 21 QVQLQWAGGGLVPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMLNHSSTLYK 80

QY 61 SALKSRSLISKDNKSNQVFLKNSLTADTAVYYCAR---KG-----EFYGYGDFVWG 112
 DB 81 TSLKSRRTISLDTSKNLFSLKSLSVTADTAVYYCARGLRGWMDVYXXGMD---VWG 137
 QY 113 QGTLVTVSS 121
 DB 138 QGTLVTVSS 146
 RESULT 7
 HV46_MOUSE STANDARD; PRT: 137 AA.
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig heavy chain V region MOPC 315 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89238351; PubMed=2497341;
 RA Rittner A., Horne C., Dorrington K.U., Klein M.;
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 RT gene segment.";
 RT Mol. Immunol. 26:431-434 (1989).
 RN [2]
 RP SEQUENCE OF 1-31.
 RX MEDLINE=78094475; PubMed=414225;
 RA Jilka R.L., Pestka S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse
 RT immunoglobulin heavy chain.";
 RT Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemlin R., Burstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors.";
 RT Fed. Proc. 38:1839-1845 (1979).
 RN [4]
 RP SEQUENCE OF 19-136.
 RX MEDLINE=74170779; PubMed=4524622;
 RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
 RT "Amino-acid sequence of the variable region of the heavy (alpha)
 RT chain of a mouse myeloma protein with anti-hapten activity.";
 RT Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
 RN [5]
 RP REVISION TO 53.
 RX MEDLINE=7244979; PubMed=268248;
 RA Hood L., Margolies M.N., Givol D., Zakut R.;
 RT Unpublished results, cited by:
 RT Padlan E.A., Davies D.R., Peck I., Givol D., Wright C.;
 RT Cold Spring Harb Symp Quant Biol. 41:627-637 (1977).
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 CC
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 CC
 CC EMBL; M27638; AAA61337.1; -;
 CC EMBL; X07880; CAA30727.1; -;
 CC PIR; P10102; AYMS35.
 CC HSSP; P01825; 7FAB.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 137
 FT DOMAIN 19 48 IG HEAVY CHAIN V REGION MOPC 315.
 FT DOMAIN 49 54 FRAMEWORK-1.
 FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 63 84 FRAMEWORK-2.
 FT DOMAIN 85 116 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 117 126 FRAMEWORK-3.
 FT DOMAIN 127 137 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G -> G (IN REF. 1; CAA30727).
 FT CONFLICT 15 15 G -> H (IN REF. 2).
 FT CONFLICT 77 78 CY -> YG (IN REF. 4).
 FT CONFLICT 102 102 N -> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON TER 137
 SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
 Query Match 56.4%; Score 365; DB 1; Length 137;
 Best Local Similarity 57.9%; Pred. No. 5,3e-31;
 Matches 70; Conservative 22; Mismatches 25; Indels 4; Gaps 2;
 QY 2 VOLKESGPIVPSQTLSTITCTISGFSL-SRYSVHWVQPPGKGLWLTGGGNTDYN 60
 DB 20 VOLKESGPIVPSQSLSTLCTGVTGYSITGFWMIKFGNKLWLGFIKYGSGNGYN 79
 QY 61 SALKSRSLISKDNKSNQVFLKNSLTADTAVYYCARKEGFYGYGDFVWGCGTLTVSS 120
 DB 80 PSLKRVSTIRDTBSNPFLLKLSVTDATVYCAQNDHLTFD---YWGQITTVS 136
 QY 121 S 121
 DB 137 S 137
 RESULT 8
 HV3H_HUMAN STANDARD; PRT: 122 AA.
 ID HV3H_HUMAN
 AC P01759;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region GA.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74175307; PubMed=4208843;
 RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
 RT Biochemistry 13:2482-2498 (1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 CC
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR; A02052; M3HUGA.
 CC HSSP; P01772; 2FB4.
 CC GO; GO:0005576; C:extracellular; NAS.
 CC GO; GO:0003823; C:antigen binding; NAS.
 CC GO; GO:0006955; P:immune response; NAS.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyrolydnone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1
 FT PYROLYDNONE CARBOXYLIC ACID.


```
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match
Best Local Similarity 54.0%; Score 349.5; DB 1; Length 122;
Matches 63; Conservative 27; Mismatches 31; Indels 1; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWYROPFGKGLFWLGMV-MGGNTDY 59
DB 1 QVQLVSGGAVZPPGSRSLRSCAAGFSFSTYAMWVQAQPGKGLZWLSVSYSGBEZTY 60
QY 60 NSALKSRSLISKNSKNQVFLKXNSLTADTAVYYCARKEGFYYGYDGFVYWGQTLTV 119
DB 1 QVQLVSGGAVZPPGSRSLRSCAAGFSFSTYAMWVQAQPGKGLZWLSVSYSGBEZTY 60
QY 120 SS 121
DB 121 SS 122

RESULT 9
HV3J_HUMAN STANDARD; PRT; 121 AA.
ID HV3J_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
RT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HLL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
[1]
SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT Biochemistry 18:553-560 (1979).
RL "Amino acid sequence of the VH region of human myeloma
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02054; GIHURL.
DR HSSP; P01772; ZFB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610E5F5AB CRC64;

Query Match
Best Local Similarity 53.9%; Score 349; DB 1; Length 121;
Matches 64; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWYROPFGKGLFWLGMV-MGGNTDY 59
DB 1 QVQLVSGGAVZPPGSRSLRSCAAGFSFSTYAMWVQAQPGKGLZWLSVSYSGBEZTY 60
QY 60 NSALKSRSLISKNSKNQVFLKXNSLTADTAVYYCARKEGFYYGYDGFVYWGQTLTV 119
DB 1 QVQLVSGGAVZPPGSRSLRSCAAGFSFSTYAMWVQAQPGKGLZWLSVSYSGBEZTY 60
QY 120 SS 121
DB 120 SS 121
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```
RESULT 10
HV2G_HUMAN STANDARD; PRT; 117 AA.
ID HV2G_HUMAN
AC P01825;
DT 21-JUL-1986 (Rel. 01, Created)
RT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region NEMM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
[1]
SEQUENCE.
RX MEDLINE=77242302; PubMed=407927;
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RT "Amino acid sequence of the VH region of a human myeloma
RL Biochemistry 16:3412-3420 (1977).
[2]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RP MEDLINE=78066916; PubMed=618887;
RA Saul F.A., Amzel L.M., Poljak R.J.;
RT "Preliminary refinement and structural analysis of the Fab fragment
RL J. Biol. Chem. 253:585-597 (1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90404; GIHURL.
DR PDB; 7FAB; 31-JAN-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyroliidone carboxylic acid.
FT DOMAIN 1 111
FT MOD_RES 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match
Best Local Similarity 53.5%; Score 346; DB 1; Length 117;
Matches 69; Conservative 22; Mismatches 25; Indels 6; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWYROPFGKGLFWLGMVGGNTDYN 60
DB 1 QVQLVSGGAVZPPGSRSLRSCAAGFSFSTYAMWVQAQPGKGLZWLSVSYSGBEZTY 60
```

QY 61 SALKSRSLSTSKDNKQVFLKNSLTAADTAAYVYCARKEGFYVYGDGFV-YMGOGTLVTVY 119
 DB 61 TPLSRVMTLVDTSKNQVSLSTLSTVTAADTAAYVYCAAN-----LIAGCIVMGOGSLTVY 115
 QY 120 SS 121
 DB 116 SS 117
 RESULT 11
 HV01_XENLA STANDARD; PRT; 136 AA.
 ID HV01_XENLA
 AC P20956;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region X1G8 precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 NC NCB1_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88176921; PubMed=2451244;
 RA Schwager J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
 RT from cDNA sequence: implications for evolution of immunoglobulin
 RT domains.";
 RT Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
 CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC DR EMBL; M20484; AAA49774.1; ALT_TERM.
 CC DR PIR; A31933; A31933.
 CC DR HSSP; P01825; 7FAB.
 CC DR InterPro; IPR007110; Ig-like.
 CC DR InterPro; IPR003596; Ig_V.
 CC DR Pfam; PF00047; Ig_1.
 CC DR SMART; SM00406; IGV_1.
 CC DR PROSITE; PS50835; IG-LIKE; 1.
 CC KW Immunoglobulin V region; Signal.
 CC FT SIGNAL 1 18
 CC FT NON TER 1
 CC FT CHAIN 19 136 IG HEAVY CHAIN V REGION X1G8.
 CC FT DOMAIN 19 128
 CC FT NON TER 136 136
 CC SQ SEQUENCE 136 AA; 15123 MW; 314183981441963 CRC64;
 Query Match 53.2%; Score 344; DB 1; Length 136;
 Best Local Similarity 53.4%; Pred. No. 8.1e-29;
 Matches 63; Conservative 24; Mismatches 29; Indels 2; Gaps 1;
 QY 4 LKESPGVIVKPSQTLSTCTISGFSLS-RYSVHWVQPPGKLEWIMGCGTNDNSL 63
 DB 21 LQESPGVIVKPSQTLSTCTISGFSLS-RYSVHWVQPPGKLEWIMGCGTNDNSL 80
 QY 64 KSRSLSTSKDNKQVFLKNSLTAADTAAYVYCARKEGFYVYGDGFVYMGOGTLVTVY 121
 DB 81 KSRVITITDNKQVFLKNSLTAADTAAYVYCARKEGFYVYGDGFVYMGOGTLVTVY 136
 RESULT 12
 HV2C_HUMAN STANDARD; PRT; 119 AA.
 ID HV2C_HUMAN

AC P01816;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region DM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCB1_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 RT heavy chains.";
 RT Biochem. J. 117:641-660(1970).
 CC -1 MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
 CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
 CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC DR PIR; A02091; GIHDM.
 CC DR HSSP; P01789; IMCP.
 CC DR GO; GO:0005376; C:extracellular; NAS.
 CC DR GO; GO:0003823; F:antigen binding; NAS.
 CC DR GO; GO:0006355; P:immune response; NAS.
 CC DR InterPro; IPR007110; Ig-like.
 CC DR InterPro; IPR003596; Ig_V.
 CC DR Pfam; PF00047; Ig_1.
 CC DR SMART; SM00406; IGV_1.
 CC DR PROSITE; PS50835; IG-LIKE; 1.
 CC KW Immunoglobulin V region; Pyrolydine carboxylic acid.
 CC FT DOMAIN 1 113
 CC FT MOD RES 1 1
 CC FT NON TER 119 119 PYROLYDINE CARBOXYLIC ACID.
 CC SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214EAD789 CRC64;
 Query Match 52.9%; Score 342; DB 1; Length 119;
 Best Local Similarity 57.6%; Pred. No. 1.1e-26;
 Matches 72; Conservative 15; Mismatches 28; Indels 10; Gaps 4;
 QY 1 QVQLKESGPGIVKPSQTLSTCTISGFSLS-RYSVHWVQPPGKLEWIMGCGTND 58
 DB 1 QVTLRESGPAIVPPTQLTLCTFSGLSGFTMCVAMIRQPPGALWLA--WDLIND 58
 QY 59 --VNSALKSRSLSTSKDNKQVFLKNSLTAADTAAYVYCARKEGFYVYGDGFVYMGOGTL 116
 DB 59 KYIASLRLAVSKDLSKQVFLKNSLTAADTAAYVYCARKEGFYVYGDGFVYMGOGTL 114
 QY 117 TVVSS 121
 DB 115 TVVSS 119
 RESULT 13
 HV61_MOUSE STANDARD; PRT; 116 AA.
 ID HV61_MOUSE
 AC P18532;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 1B43 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALB/cJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response.";
 RT J. Exp. Med. 165:2007-2018(1989).
 CC -1 MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.

DR PIR; JTO508; HWS1B.
 DR PDB; 1KCS; 11-MAY-02.
 DR PDB; 1KCV; 11-MAY-02.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; signal; 3D-structure.
 FT CHAIN 1 18
 FT SIGNAL 18
 FT DOMAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
 FT DOMAIN 19 48 FRAMEWORK-1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 54 67 FRAMEWORK-2.
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DISULFID 40 114 BY SIMILARITY.
 FT NON TER 116
 SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 52.3%; Score 338.5; DB 1; Length 116;
 Best Local Similarity 64.9%; Pred. No. 2.5e-28;
 Matches 63; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 2 VOLKESGPGVLPSPQTLSTCTTISGFSL-SRYSVHWVRQPPKGLGMLGMIWGAGNTDYN 60
 DB 20 VOLKESGPGVLPSPQSLSTCTTCTVGTGYSITSGSWHMIRQFQNKLEWMIYIHSGNTSYN 79

QY 61 SALKSRSLISKDMSKNQVFLKNSLTADTAAYVCAR 97
 DB 80 PSLKSRISITRDTSKNOFLQANSVTEDTAAYVCAR 116

RESULT 14
 HV3K HUMAN STANDARD; PRT; 129 AA.
 ID HV2F HUMAN P01824;
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region WAH.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Telaar D., Debutre B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02093; D2HWA.
 DR HSSP; P01825; 7FAB.
 DR GLYCOSITE; P01824; -.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 113 IG-LIKE.
 FT NON TER 129
 SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE5119 CRC64;

Query Match 52.2%; Score 338; DB 1; Length 129;
 Best Local Similarity 53.5%; Pred. No. 3.2e-28;

Matches 69; Conservative 21; Mismatches 31; Indels 8; Gaps 3;

QY 1 QVOLKESGPGVLPSPQTLSTCTTISGFSLSR--SVHWVRQPPKGLGMLGMIWGAGNTD 58
 DB 1 RLQLOESGPGVLPSPQTLSTCTTISGFSLSR--SVHWVRQPPKGLGMLGMIWGAGNTD 60

QY 59 YNSALKSRSLISKDMSKNQVFLKNSLTADTAAYVCAR-KGEFYGYG-----DGFVWG 112
 DB 61 YNPSLKGRVTLISVDSIRQFSLNLSMAADTAAYVCARGNPPPYDICTGSDGIDVWG 120

QY 113 QGTLVTVSS 121
 DB 121 QGTLVTVSS 129

RESULT 15
 HV3K HUMAN STANDARD; PRT; 126 AA.
 ID HV3K HUMAN P01772;
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region KOL.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE AND DISULFIDE BONDS.
 RA MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE=81072295; PubMed=7441755;
 RA Maquart M., Delsenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR; A02055; GHUKY.
 DR PDB; 2PB4; 12-JUL-89.
 DR PDB; 2IG2; 12-JUL-89.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 FT CHAIN 1 112
 FT SIGNAL 112
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT STRAND 29 31
 FT HELIX 31 39
 FT STRAND 34 39
 FT TURN 41 42
 FT STRAND 45 51
 FT TURN 53 54
 FT STRAND 58 60
 FT STRAND 62 64
 FT HELIX 64 65
 FT STRAND 65 65
 FT TURN 66 67
 FT STRAND 68 73

FT	TURN	74	77
FT	STAND	8	83
FT	HELI	88	50
FT	STAND	92	99
FT	STAND	106	166
FT	TURN	107	108
FT	STAND	109	109
FT	STAND	109	163
FT	STAND	113	166
FT	STAND	120	124
FT	NON TER	166	166
SEQ	SEQUENCE	126 AA:	133

Query Match	51.9%	Score 335.5	DB 1	Length 126
Best Local Similarity	51.9%	Pred. No. 5.7e+28		
Matches 68	Conservative 22	Mismatches 26		Indels 15
				Gaps 4

```

QY 1 QVQLKESGPELVPSQSLTSTCTISGEFLSPRYSHWVQPPKGLIEWLGMV--GGAGNTDY 59
Db 1 QVQLVVEGGGVAVOPGKRLRLSCSSGCFITSSYAMVWVQAPKGLIEWALLIWDGSDQHY 60
QY 60 NSALKSELSTLSKNSKNQVFLKNSLPTAADTAVYCARKEERYGYDGFV-----Y 110
Db 61 ADSYKGFITSRDNSKNITFLQMDSLRPEDTGVYFCARDG-----GH-GFCSSASGCFPDY 115
QY 111 WGQGLTIVSS 121
Db 116 WGQGLTIVSS 126

```

Search completed: March 26, 2004, 05:04:47
Job time : 8.29433 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:13 ; Search time 34.9699 Seconds
(without alignments)
1091.732 Million cell updates/sec

Title: US-10-056-052a-20

Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSQTLSTI.....YYGNDGFPVWGQGLTVWSS 121

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	465.5	71.9	121	11 Q99NG4	Q99NG4 mus musculus
2	463.5	71.6	482	11 Q91X92	Q91X92 mus musculus
3	413	63.8	119	4 Q9UL73	Q9UL73 homo sapien
4	402.5	62.2	613	4 Q96EX0	Q96EX0 homo sapien
5	385.5	59.6	496	4 Q96KX8	Q96KX8 homo sapien
6	382.5	59.1	118	11 Q811U5	Q811U5 mus musculus
7	382.5	59.1	478	4 Q7Z379	Q7Z379 homo sapien
8	382	59.0	492	4 Q7Z374	Q7Z374 homo sapien
9	373.5	57.7	150	4 Q95973	Q95973 homo sapien
10	369	57.0	479	11 Q99W22	Q99W22 mus musculus
11	368	56.9	139	4 Q86SX2	Q86SX2 homo sapien
12	363.5	56.2	573	4 Q8WU38	Q8WU38 homo sapien
13	363	56.1	121	4 Q8UT96	Q8UT96 homo sapien
14	359	55.5	121	4 Q8UL71	Q8UL71 homo sapien
15	355.5	54.9	613	4 Q8WUK1	Q8WUK1 homo sapien
16	355	54.9	493	4 Q8NCU6	Q8NCU6 homo sapien

17	354	54.7	588	4 Q8WUX4	Q8WUX4 homo sapien
18	354	54.7	597	4 Q9BU10	Q9BU10 homo sapien
19	354	54.7	618	4 Q96XA6	Q96XA6 homo sapien
20	352.5	54.5	130	4 Q812D7	Q812D7 homo sapien
21	351	54.3	116	4 Q9UL93	Q9UL93 homo sapien
22	350.5	54.2	122	4 Q9UL75	Q9UL75 homo sapien
23	350.5	54.2	147	4 Q9Y509	Q9Y509 homo sapien
24	350	54.1	597	4 Q9BQ08	Q9BQ08 homo sapien
25	350	54.1	597	4 Q9E8B9	Q9E8B9 homo sapien
26	346.5	53.6	499	11 Q8R3V9	Q8R3V9 mus musculus
27	345.5	53.4	473	4 Q8TC63	Q8TC63 homo sapien
28	344	53.2	113	4 Q9UL90	Q9UL90 homo sapien
29	343.5	53.1	112	4 Q9HCC1	Q9HCC1 homo sapien
30	337.5	52.2	118	4 Q9UL72	Q9UL72 homo sapien
31	337	52.1	119	11 Q920E7	Q920E7 mus musculus
32	336	51.9	473	11 Q9D8L4	Q9D8L4 mus musculus
33	334.5	51.7	116	4 Q7Z3Y6	Q7Z3Y6 homo sapien
34	333	51.5	131	4 Q9UL88	Q9UL88 homo sapien
35	332.5	51.4	122	4 Q9UL84	Q9UL84 homo sapien
36	331.5	51.2	487	11 Q93XA4	Q93XA4 mus musculus
37	330.5	51.1	298	11 Q9QYF0	Q9QYF0 mus musculus
38	324.5	50.2	470	4 Q7Z5W1	Q7Z5W1 homo sapien
39	322	49.8	470	4 Q8NSK4	Q8NSK4 homo sapien
40	321	49.6	499	4 Q9UL91	Q9UL91 homo sapien
41	319.5	49.4	118	4 Q9UL91	Q9UL91 homo sapien
42	319.5	49.4	136	11 Q7TPE3	Q7TPE3 mus musculus
43	318.5	49.2	484	11 Q8VEA0	Q8VEA0 mus musculus
44	317.5	49.1	124	6 Q9N0W6	Q9N0W6 cryotolagus
45	316.5	48.9	124	6 Q9N0W4	Q9N0W4 cryotolagus

ALIGNMENTS

RESULT 1

Q99NG4 ID Q99NG4 PRELIMINARY: PRT: 121 AA.
AC Q99NG4
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Plasmid phn1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=9816918; PubMed=9510199;
RA Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
RT Baensch W., Kola A., Klos A., Koehn J.,
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries."
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -
DR PIR; F33933; F33932.
DR HSSP; P01825; 7PAB.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PSS0835; IG_Like; 1.
KW plasmid.
DR NON_TER 1
FT NON_TER 1
SQ
SEQUENCE 121 AA; 1325 MW; D293EABBC8C9D5B CRC64;
Query Match 71.9%; Score 465.5; DB 11; Length 121;
Best Local Similarity 74.0%; Pred. No. 6.5e-43;
Matches 91; Conservative 9; Mismatches 18; Indels 5; Gaps 2;

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QY 1 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 60
DB 1 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 60
QY 61 SALKSRSLISKDNKSNQVFLKMSLTADTAIVVYCARKEFF--YGYDGFVYWGQTLVT 118
DB 61 SALKSRSLISKDNKSNQVFLKMSLTADTAIVVYCARKEFF--YGYDGFVYWGQTLVT 117
QY 119 VSS 121
DB 118 VSS 120

RESULT 2
Q91X92 PRELIMINARY; PRT; 482 AA.
ID Q91X92
AC Q91X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011181; AAI11181.1; -
DR EPR; F33932; F33932.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003036; IG_MHC.
DR Pfam; PFO0047; IG_4.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
DR Hypothetical protein.
KW SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;
SQ

Query Match 71.6%; Score 463.5; DB 11; Length 482;
Best Local Similarity 74.6%; Pred. No. 6,2e-42;
Matches 91; Conservative 11; Mismatches 15; Indels 5; Gaps 2;

QY 1 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 60
DB 20 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 79
QY 61 SALKSRSLISKDNKSNQVFLKMSLTADTAIVVYCARKEFF--YGYDGFVYWGQTLVT 119
DB 80 SALKSRSLISKDNKSNQVFLKMSLTADTAIVVYCARKEFF--YGYDGFVYWGQTLVT 135
QY 120 SS 121
DB 136 SS 137

RESULT 3
Q9UL73 PRELIMINARY; PRT; 119 AA.
ID Q9UL73
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035041; AAD56277.1; -
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PFO0047; IGV; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

Query Match 63.8%; Score 413; DB 4; Length 119;
Best Local Similarity 65.9%; Pred. No. 3,4e-37;
Matches 81; Conservative 16; Mismatches 20; Indels 6; Gaps 2;

QY 1 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 60
DB 1 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 60
QY 61 SALKSRSLISKDNKSNQVFLKMSLTADTAIVVYCARKEFF--YGYDGFVYWGQTLVT 118
DB 61 SALKSRSLISKDNKSNQVFLKMSLTADTAIVVYCARKEFF--YGYDGFVYWGQTLVT 116
QY 119 VSS 121
DB 117 VSS 119

RESULT 4
Q96EY0 PRELIMINARY; PRT; 613 AA.
ID Q96EY0
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011857; AAI1857.1; -
DR EPR; S15590; S15590.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003036; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PFO0047; IGV; 5.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
DR Hypothetical protein.
KW SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
SQ

Query Match 62.2%; Score 402.5; DB 4; Length 613;
Best Local Similarity 64.5%; Pred. No. 3,8e-35;
Matches 78; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

QY 1 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 60
DB 20 QVOLKESGPGVLVKSQTLSTCTTSGFSLRSYVHWVROPKGLKLEWLMGIMGGNTDYN 79
QY 61 SALKSRSLISKDNKSNQVFLKMSLTADTAIVVYCARKEFF--YGYDGFVYWGQTLVT 120
```

Db 80 PSLAKSVTMSVDTSKQPSLKLSVTADTAITYYCAQG-PWELPVLGFLFYMGCGTLVTS 138
 QY 121 S 121
 Db 139 S 139

RESULT 5

ID	Q96KX8	PRELIMINARY;	PRT;	496 AA
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DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAL16369.1; -
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CEC64;

Query Match	Score	DB 4	Length
59.6%	385.5	4	496

Best Local Similarity 62.9%; Pred. No. 2,18-33;
Matches 78; Conservative 18; Mismatches 25; Indels 3; Gaps 2

[illegible]

RESULT 6

ID	PRELIMINARY;	PRT;	118 AA
Q81105			
Q81106			

DT 01-JUN-2003 (Tremblrel, 24, Created)
 DT 01-JUN-2003 (Tremblrel, 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel, 25, Last annotation update)
 DE Anti-human Fc gamma receptor III 368 gamma heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/c;
 RA Bruenke J., Valerius T., Repp R., Fey G.H.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AY153025; AAC18227.1; -;
 GO GO:0004872; F:receptor activity; IEA.

DR	InterPro: IPRO03599; IG_	1ike.
DR	InterPro: IPRO07110; IG_	1like.
DR	InterPro: IPRO03596; IG_	v.
DR	Pfam: PF00047; IG; 1.	
DR	SMART: SMO0409; IG; 1.	
DR	SMART: SMO0406; IGv; 1.	
DR	PROSITE: PS00835; IG_Like; 1.	
KM	Receptor.	
FT	NON_TER	1
FT	NON_TER	118
SC	SEQUENCE	116 AA; 12979 MM; F57BB0703742E89 CRC64;

Query Match	59.1%;	SCORE 382.5;	DB II;	length 116;
Best Local Similarity	62.6%;	Pred. No. 7.2e-34;		
Matches 77;	Conservative 13;	Mismatches 26;	Indels 7;	Gaps 2

[illegible]

RESULT 7

ID	Q7Z379	PRELIMINARY;	PRT;	478	AA
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DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp668K04218 (Fragment).
GN DKFZp668K04218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
[1]_TaxID=9606;
RP TISSUE FROM N.A.
RC SKELE-Human rectum tumor;
RA Blesoecker H., Boecker M., Mewes H.W., Weill B., Amlid C., Osanger A
RA Foto G., Han N., Nishimura S., EMBL/Genbank/DBJ databases.
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; BX538066; CAD97936.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 5620 MW; 4AFCB541F3217CA1 CRC64;

Query Match	59.1%	Score	38.5	DB 4	Length	770			
Best Local Similarity	63.4%	Pred. No.	4.2e-33						
Matches	78	Conservative	16	Mismatches	24	Indels	5	Gaps	2

QY 1 QVQIKKEGPELTVRSGTSLITCTIGGFSLSR--YVHWVRQPEPQNGLEMLMTMGAGNL 36
 Db 19 QVQIQEGSGPELTVRSGTSLITCTVGGSGISGSDYFMWIRQAPRGLEMMGYIYSGSTY 78
 QY 59 YNSALKRRSLISKQNSKNOVFLQMSLTADTAVYAKRKPEFYVGDGPFYWGQGLLT 118
 Db 79 YNPSELRSLISIDTKNQFSLRNSLTADTAVYFCRGVGLTADF--TWQGVVVT 135

QY	119	VSS	121
Db	136	VSS	138

RESULT 8	
Q72374	
ID Q72374	PRELIMINARY; PRT; 492 AA

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AC 072374;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN DKFZp686C02218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Boecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX538077; CAD98001.1; -.
KM Hypothetical protein.
FT NON_PTB
SQ SEQUENCE 492 AA; 5376 MW; 1E7A15760F0CA74B CRC64;

Query Match
Best Local Similarity 59.0%; Score 382; DB 4; Length 492;
Matches 78; Conservative 16; Mismatches 25; Indels 4; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLS--RYSVHWYRQPPGKLEWLGIMWGND 58
DB 32 QLOLQESGPGLVKPSSETLSLTCTVSGSVSNRMVGMWIKQPGKLEWLGISTVYNT 91
QY 59 YNSALKRSLSTSKNSKNOVFLKNSLTADTAVVYCARKEFYGYDGFFVYGGGLTY 118
DB 92 YSPSLKRLITPVDTSKNHPSLRITSTADTAVVYVVRVVEGYGM--FDPMGGGLTY 149
QY 119 VSS 121
DB 150 VSS 152

RESULT 9
Q95973 PRELIMINARY; PRT; 150 AA.
AC 095973;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
RT Behcet's patient with arthritis."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF103795; AAC79084.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM SIGNAL.
FT CHAIN 1
FT NON_TER 20 >150
SQ SEQUENCE 150 AA; 16315 MW; 85664E0438AA7C9 CRC64;

Query Match
Best Local Similarity 57.7%; Score 373.5; DB 4; Length 150;
Matches 73; Conservative 20; Mismatches 23; Indels 7; Gaps 2;

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QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLS--RYSVHWYRQPPGKLEWLGIMWGND 58
DB 20 QLOLQESGPGLVKPSSETLSLTCTVSGSVSNRMVGMWIKQPGKLEWLGISTVYNT 79
QY 59 YNSALKRSLSTSKNSKNOVFLKNSLTADTAVVYCARKEFYGYDGFFVYGGGLTY 118
DB 80 YNSPLKRLITPVDTSKNHPSLRITSTADTAVVYCAR-----LDMGAFDFMGHGMV 134
QY 119 VSS 121
DB 135 VSS 137

RESULT 10
Q99W22 PRELIMINARY; PRT; 479 AA.
ID 099W22;
AC 099W22;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strassberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002091; AAH02091.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match
Best Local Similarity 57.0%; Score 369; DB 11; Length 479;
Matches 71; Conservative 22; Mismatches 22; Indels 6; Gaps 2;

QY 2 VOLKESGPGLVKPSQTLSTCTISGFSLS--RYSVHWYRQPPGKLEWLGIMWGND 60
DB 20 VOLQESGPGLVKPSQSLTCTVSGSVSNRMVGMWIKQPGKLEWLGISTVYNT 79
QY 61 SALKRSLSTSKNSKNOVFLKNSLTADTAVVYCARKEFYGYDGFFVYGGGLTY 120
DB 80 PSFKRSLITPVDTSKNHPSLRITSTADTAVVYCAR-----GYSPFNNGGLTY 134
QY 121 S 121
DB 135 A 135

RESULT 11
Q86SX2 PRELIMINARY; PRT; 139 AA.
ID 086SX2;
AC 086SX2;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CS0DU004YM19 of B cells (Ramos cell line)
DE of Homo sapiens (Human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RC Tissue=B-cell;
RA Genoscope;
RU Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=B-cell;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization";
RU Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX248300; CAC62627.1; -
DR GO: 0045821; Cerebrachromosomal DNA; IEA.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; Ig_Like; 1.
DR Plasmaid.
KW NON_TER
FT
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 56.9%; Score 368; DB 4; Length 139;
Best Local Similarity 70.1%; Pred. No. 3.4e-32;
Matches 68; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWTRPPGKGLGLMTGGGNTDYN 60
Db 33 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWTRPPGKGLGLMTGGGNTDYN 92
61 SALKSRLLSKNSKNSKQVFLKNSLTADTAVYYCAR 97
93 PSLKSRVLTISVDTSKQPSIKLSVTADTAVYYCAR 129

RESULT 12
Q8WU38 PRELIMINARY; PRT; 573 AA.
AC 08WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Tonsil;
RA Strausberg R.;
RU Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC021276; AAH21276.1; -
DR FIR; S21205; S21205.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; Ig_Like; 4.
DR PROSITE: PS00290; Ig_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 56.2%; Score 363.5; DB 4; Length 573;
Best Local Similarity 53.5%; Pred. No. 6.3e-31;
Matches 66; Conservative 23; Mismatches 27; Indels 9; Gaps 3;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWTRPPGKGLGLMTGGGNTDYN 59
Db 20 EVQLVESGGGLVOPGRSLRLSCAASGFTPDYAMHWYRQAPGKLEWVSIGNSISIGY 79

QY 60 NSALKSRLLSKNSKNSKQVFLKNSLTADTAVYYCARKE-----FYVGGDFVYWGOG 114
Db 80 ADSVKGKRFISRNANNSLYLQNNSLPADTALYICAGKSGSYIGYIGMD---VWGOG 136

QY 115 TLTVVSS 121
Db 137 TLTVVSS 143

RESULT 13
Q9UL96 PRELIMINARY; PRT; 121 AA.
ID Q9UL96
AC Q9UL96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035018; AA056254.1; -
DR HSSP: P01825; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; Ig_Like; 1.
DR NON_TER
FT NON_TER
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 56.1%; Score 363; DB 4; Length 121;
Best Local Similarity 60.0%; Pred. No. 1e-31;
Matches 75; Conservative 15; Mismatches 27; Indels 8; Gaps 3;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWTRPPGKGLGLMTGGGNTD 58
Db 1 QITLKESGPTLVKPTQTLTCTISGFSLSRYSVHWTRPPGKGLGLMTGGGNTD 60
59 YNSALKSRLLSKNSKNSKQVFLKNSLTADTAVYYCAR--RKEFFYGYGDFVYWGOGTL 116
61 YSPSLKSRLLITTKDTSKNSQVLTFTFMDPWTATVYCARHRSKSGDY----FDYWGQGL 116

QY 117 TVVSS 121
Db 117 TVVSS 121

RESULT 14
Q9UL71 PRELIMINARY; PRT; 121 AA.
ID Q9UL71
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PR0003596; IG_v.
 DR SMART; SM00406; IG_v.1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 FT NON TER 1
 FT 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CFA5D50736 CRC64;

Query Match 55.5%; Score 359; DB 4; Length 121;
 Best Local Similarity 57.4%; Pred. No. 2.7e-31;
 Matches 70; Conservative 21; Mismatches 29; Indels 2; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTICRTISGFSLSRYSVHWVROPKGLKWLGMWG-GNTDY 59
 Db 1 EVQLVESGGGVVQPGSGSLRLFCASGFTPDGYAMHWVROAPKGLKLVWVSLISGDGSGTYY 60
 QY 60 NSALKSLSTKDKNSKQVFLKMSLTADTAVYYCAKRGKGFYGYDGFTYMGQGLTVTV 119
 Db 61 ADSVKGRTISRDKNSKNTLYIQNMSLRAPDTAVYYCA-KGKVTITTYDFDIWGQGLTVTV 119
 QY 120 SS 121
 Db 120 SS 121

RESULT 15

Q8WUK1 PRELIMINARY; PRT; 613 AA.
 AC Q8WUK1;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=tonsil;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC020240; AA020240.1; -.
 DR PIR; P01320; P01320.
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 5.
 DR SMART; SM00406; IG_v.1.
 DR PROSITE; PS50835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KM Hypothetical protein.
 SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 54.9%; Score 355.5; DB 4; Length 613;
 Best Local Similarity 55.7%; Pred. No. 5.1e-30;
 Matches 68; Conservative 23; Mismatches 28; Indels 3; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTICRTISGFSLSRYSVHWVROPKGLKWLGMWG-GNTDY 59
 Db 20 QVQLVESGGGVVQPGSGSLRLFCASGFTPDGYAMHWVROAPKGLKLVWVSLISGDGSGTYY 79
 QY 60 NSALKSLSTKDKNSKQVFLKMSLTADTAVYYCAKRGKGFYGYDGFTYMGQGLTVTV 119

Db 80 ADSVKGRTISRDKNSKNTLYIQNMSLRAPDTAVYYCAK--DMSGVEFTFDIWGQGLTVTV 137
 QY 120 SS 121
 Db 138 SS 139

Search completed: March 26, 2004, 05:07:48
 Job time : 36.9699 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:51:26 ; Search time 6.75177 Seconds
(without alignments)
863.752 Million cell updates/sec

Title: US-10-056-052a-18

Perfect score: 583
Sequence: 1 DIVMGPSPDLSAVSLGERVT.....YCHOYLSSTFGGKTLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	521	89.4	133	KV4B_HUMAN	P06313 homo sapien
2	520.5	89.3	114	KV4A_HUMAN	P06312 homo sapien
3	505.5	86.7	134	KV4C_HUMAN	P06314 homo sapien
4	479	82.2	121	KV4D_HUMAN	P06312 homo sapien
5	467.5	80.2	109	KV4B_HUMAN	P06313 homo sapien
6	388.5	66.6	136	KV3B_MOUSE	P01634 mus musculu
7	387	66.4	110	KV3P_MOUSE	P01668 mus musculu
8	384.5	66.0	111	KV3I_MOUSE	P01668 mus musculu
9	381	65.4	129	KV3I_HUMAN	P18135 homo sapien
10	381	65.4	129	KV3M_HUMAN	P18136 homo sapien
11	379.5	65.1	149	KV5A_MOUSE	P01633 mus musculu
12	377	64.7	109	KV3B_HUMAN	P01620 homo sapien
13	376	64.5	109	KV3D_HUMAN	P01622 homo sapien
14	375.5	64.4	114	KV1A_MOUSE	P01632 mus musculu
15	374.5	64.2	108	KV1M_HUMAN	P01605 homo sapien
16	374	64.2	109	KV3E_HUMAN	P01623 homo sapien
17	373.5	64.1	111	KV3M_MOUSE	P01665 mus musculu
18	373.5	64.1	111	KV3O_MOUSE	P01667 mus musculu
19	372.5	63.9	111	KV3H_MOUSE	P01660 mus musculu
20	372	63.8	129	KV3H_HUMAN	P04207 homo sapien
21	367.5	63.0	111	KV3N_MOUSE	P01666 mus musculu
22	367.5	63.0	111	KV3R_MOUSE	P01670 mus musculu
23	367.5	63.0	129	KV1W_HUMAN	P04431 homo sapien
24	367	63.0	108	KV3A_HUMAN	P01624 homo sapien
25	367	63.0	109	KV3F_HUMAN	P01624 homo sapien
26	366.5	62.9	111	KV3J_MOUSE	P01662 mus musculu
27	366	62.9	133	KV2F_HUMAN	P06310 homo sapien
28	365.5	62.7	111	KV3Q_MOUSE	P01669 mus musculu
29	365.5	62.7	111	KV3U_MOUSE	P01673 mus musculu
30	365	62.6	113	KV2G_HUMAN	P01615 homo sapien
31	365	62.6	113	KV2G_MOUSE	P01631 mus musculu
32	364.5	62.5	108	KV1V_HUMAN	P04430 homo sapien
33	364.5	62.5	108	KV1Y_HUMAN	P03062 homo sapien

34	364.5	62.5	115	1	KV2A_HUMAN	P01614 homo sapien
35	364	62.4	117	1	KV2E_HUMAN	P06309 homo sapien
36	362.5	62.2	108	1	KV1H_HUMAN	P01600 homo sapien
37	362	62.1	107	1	KV1D_HUMAN	P01596 homo sapien
38	362	62.1	109	1	KV3G_HUMAN	P04306 homo sapien
39	361.5	62.0	131	1	KV3I_MOUSE	P01661 mus musculu
40	360.5	61.8	108	1	KV1C_HUMAN	P01603 homo sapien
41	360.5	61.8	108	1	KV1O_HUMAN	P01607 homo sapien
42	360.5	61.8	111	1	KV3S_MOUSE	P01671 mus musculu
43	360.5	61.8	128	1	KV3K_HUMAN	P06311 homo sapien
44	359	61.6	113	1	KV2D_HUMAN	P01617 homo sapien
45	358.5	61.5	111	1	KV3T_MOUSE	P01672 mus musculu

ALIGNMENTS

RESULT 1
KV4B_HUMAN STANDARD; PRT; 133 AA.
ID KV4B_HUMAN
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-IV region VJ precursor.
RT Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=8604183; PubMed=297712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
RT Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene".
RL Nucleic Acids Res. 13:6515-6523(1985).

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CC entities requires a license agreement (See <http://www.ibt-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL; Z00022; CAA7317.1; -.
DR PIR; A01904; K4HUJ1.
DR HSSP; P80362; IWTJ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;
Query Match 89.4%; Score 521; DB 1; Length 133;
Best Local Similarity 89.3%; Pred. No. 1.5e-48;

Matches 100; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTNCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60
DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNVYLAWYQKPGQSPKLLIYMASTR 80

QY 61 ESGVPRFSGSGSGTDTFTLTISLQAEADVAVYCCQYDTPFGGATKVEIK 112
DB 81 ESGVPRFSGSGSGTDTFTLTISLQAEADVAVYCCQYDTPFGGATKVEIK 132

RESULT 2
KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P0635;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
DR PDB; 1EEB; 01-FEB-01.
DR PDB; 1EBU; 03-FEB-01.
DR PDB; 1ERQ; 09-FEB-01.
DR PDB; 1EK3; 06-MAR-01.
DR PDB; 1LVE; 21-JAN-98.
DR PDB; 3LVE; 18-MAY-99.
DR PDB; 3LVE; 28-MAR-01.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 41 55 FRAMEWORK-2.
FT DOMAIN 4 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 63 62 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 6 95 101 FRAMEWORK-3.
FT DOMAIN 7 102 113 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 102 113 FRAMEWORK-4.
FT NON TER 114 BY SIMILARITY.
FT SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 89.3%; Score 520.5; DB 1; Length 114;
Best Local Similarity 89.4%; Pred. No. 1.4e-48;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERVTNCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNVYLAWYQKPGQSPKLLIYMASTR 60

QY 61 ESGVPRFSGSGSGTDTFTLTISLQAEADVAVYCCQYDTPFGGATKVEIK 112
DB 81 ESGVPRFSGSGSGTDTFTLTISLQAEADVAVYCCQYDTPFGGATKVEIK 112

DB 61 ESGVPRFSGSGSGTDTFTLTISLQAEADVAVYCCQYDTPFGGATKVEIK 113

RESULT 3
KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1998 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; X02990; CAA26733.1; -
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 1 21 43 FRAMEWORK-1.
FT DOMAIN 2 21 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 4 61 75 FRAMEWORK-2.
FT DOMAIN 5 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 6 83 114 FRAMEWORK-3.
FT DOMAIN 7 115 121 FRAMEWORK-4.
FT DOMAIN 8 122 133 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 134
FT SEQUENCE 134 AA; 14966 MW; 6413A22F0D738832 CRC64;

Query Match 86.7%; Score 505.5; DB 1; Length 134;
Best Local Similarity 85.8%; Pred. No. 6.7e-47;
Matches 97; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERVTNCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60
DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNVYLAWYQKPGQSPKLLIYMASTR 80

QY 61 ESGVPRFSGSGSGTDTFTLTISLQAEADVAVYCCQYDTPFGGATKVEIK 112
DB 81 ESGVPRFSGSGSGTDTFTLTISLQAEADVAVYCCQYDTPFGGATKVEIK 133

RESULT 4

KV40 HUMAN STANDARD; PRT; 121 AA.

AC P06312:

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE IG kappa chain V-IV region precursor (Fragment).

GN IGKV4-1.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

CC NCBI_TaxID=9606;

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041853; PubMed=2997712;

RA Kloeck H.G., Bornkamm G.W., Combiato G., Mocikat R., Pohlenz H.D., Zachau H.G.,

RT "Subgroup IV of human immunoglobulin K light chains is encoded by a single germline gene."

RL Nucleic Acids Res. 13:6515-6529(1985).

CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.

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CC CC

DR EMBL; Z00023; CAA77318.1; -.

DR PIR; A01902; K4HU.

DR HSP; P80362; 1WTU.

DR Genew; HGNC:5834; IGKV4-1.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003596; IG_v.

DR Pfam; PF00047; IG_1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region; Signal.

KW SIGNAL

FT CHAIN 1 20

FT DOMAIN 21 >121 IG KAPPA CHAIN V-IV REGION.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 61 75 FRAMEWORK-2.

FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 83 114 FRAMEWORK-3.

FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 43 114 BY SIMILARITY.

FT NON TER 121

SEQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 82.2%; Score 479; DB 1; Length 121;

Best Local Similarity 91.0%; Pred. No. 4e-44;

Matches 91; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSGERYTANCKSSQSVLYSSNNKNTLAWYQKQKGPCKLLIYMASTR 60

DB 21 DIVMTQSPDLSAVSGERYTANCKSSQSVLYSSNNKNTLAWYQKQKGPCKLLIYMASTR 80

QY 61 ESGVDPDFSGSGSGTDFTLTISVQAEDLAVYYCHQYLS 100

DB 81 ESGVDPDFSGSGSGTDFTLTISVQAEDLAVYYCHQYLS 120

RESULT 5

KV4D HUMAN STANDARD; PRT; 109 AA.

ID KV4D HUMAN

AC P83593;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE IG kappa chain V-IV region 5TH (Fragment).

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

CC NCBI_TaxID=9606;

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RC TISSUE=Abdominal adipose tissue;

RX MEDLINE=98249779; PubMed=9588180;

RA Olsen K.E., Sletten K., Westermarck P.;

RT "Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain."

RL Biochem. Biophys. Res. Commun. 245:713-716(1998).

CC -1- FUNCTION: May play an important role in fibrillogenesis.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003599; IG.

DR InterPro: IPR003596; IG_v.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region.

FT CHAIN 1 23

FT DOMAIN 24 40 FRAMEWORK-1.

FT DOMAIN 41 55 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 63 94 FRAMEWORK-3.

FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 102 109 FRAMEWORK-4.

FT DISULFID 23 94 BY SIMILARITY.

FT UNSURE 23 23

FT UNSURE 94 94

FT NON TER 109 109

SEQ SEQUENCE 109 AA; 12060 MW; 0C4F31E1A11E12A0B CRC64;

Query Match 80.2%; Score 467.5; DB 1; Length 109;

Best Local Similarity 82.6%; Pred. No. 5.9e-43;

Matches 90; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVMTQSPDLSAVSGERYTANCKSSQSVLYSSNNKNTLAWYQKQKGPCKLLIYMASTR 60

DB 1 DIVMTQSPDLSAVSGERYTANCKSSQSVLYSSNNKNTLAWYQKQKGPCKLLIYMASTR 60

QY 61 ESGVDPDFSGSGSGTDFTLTISVQAEDLAVYYCHQYLS-SYTFGGGTX 108

DB 61 ESGVDPDFSGSGSGTDFTLTISVQAEDLAVYYCHQYLS-SYTFGGGTX 109

RESULT 6

KV5B MOUSE STANDARD; PRT; 136 AA.

ID KV5B MOUSE

AC P01634;

DT 21-JUN-1986 (Rel. 01, Created)

DT 21-JUN-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE IG kappa chain V-V region MOPC 21 precursor.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82059477; PubMed=6170937;

RA Hamlyn P.H., Galt M.J., Milstein C.;

RT "Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing."

RL Nucleic Acids Res. 9:4485-4494(1981).

RN [2]

RP SEQUENCE OF 30-136.

RX MEDLINE=73053310; PubMed=4638343;

RA Svasti J., Milstein C.;

RT "The complete amino acid sequence of a mouse kappa light chain."
 RL Biochem. J. 128:427-444(1972).
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 CC -----
 CC EMBL: V00810; CA24192.1; ALT_TERM.
 DR PIR: A93736; KYMS21.
 DR PDB: 1IGC; 03-JUN-95.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal; 3d-structure.
 FT SIGNAL 1 29
 FT CHAIN 1 136 IG KAPPA CHAIN V-V REGION MOPC 21.
 FT DOMAIN 30 136 FRAMEWORK-1.
 FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 64 78 FRAMEWORK-2.
 FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 127 136 FRAMEWORK-4.
 FT NON_TER 126 136
 FT SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;
 SQ
 Query Match 66.6%; Score 388.5; DB 1; Length 136;
 Best Local Similarity 69.0%; Pred. No. 2e-34;
 Matches 78; Conservative 15; Mismatches 13; Indels 7; Gaps 2;
 QY 1 DIVVTGSPDLSAVLSGERVTMNCSSQSVLYSSNOKNYLAWYQKRGQSPKLLIYMASTR 60
 DB 30 NIVMTGSPKMSMSVSEKVTLTCKASENVV-----TVSYWYQKKEQSPKLLIYGASNR 83
 QY 61 ESGVDPDFSGSGGSDTFTLTISVQAEADLAVVYCHQ-YLSSYFGGSKLEIK 112
 DB 84 YTGVPDRFTGSSGSDTFTLTISVQAEADLAVVYCHQYGYPTFGGSKLEIK 136
 RESULT 7
 KVP3_MOUSE STANDARD; PRT; 110 AA.
 ID KVP3_MOUSE
 AC P01668;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Ig kappa chain V-III region PC 7210.
 DS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattalman L., Ioh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity."
 RL Nature 276:785-790(1978).
 RL PIR: D01937; KYMS10.
 DR HSSP: P01679; 2FBI.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT SEQUENCE

FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 101 110 FRAMEWORK-4.
 FT DISULFID 101 110 BY SIMILARITY.
 FT NON_TER 110 110
 FT SEQUENCE 110 AA; 11950 MW; 69F1A5CE868B1249 CRC64;
 SQ
 Query Match 66.4%; Score 387; DB 1; Length 110;
 Best Local Similarity 67.9%; Pred. No. 2.3e-34;
 Matches 76; Conservative 12; Mismatches 22; Indels 2; Gaps 1;
 QY 1 DIVVTGSPDLSAVLSGERVTMNCSSQSVLYSSNOKNYLAWYQKRGQSPKLLIYMASTR 60
 DB 1 DIVLTGSPASLAVSLGKATISCAQSDLYDD--SYNMWYQKRGQSPKLLIYASNL 58
 QY 61 ESGVDPDFSGSGGSDTFTLTISVQAEADLAVVYCHQYLSYFGGSKLEIK 112
 DB 59 ESGVPDRFTGSSGSDTFTLTINHPVEEDATYCHQSEDPWTGSGTLEIK 110
 RESULT 8
 KVP3_MOUSE STANDARD; PRT; 111 AA.
 ID KVP3_MOUSE
 AC P01664;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Ig kappa chain V-III region CBPC 101.
 DS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions."
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -I-MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR: A01936; KYMS1.
 DR HSSP: P80362; 1MTL.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 FRAMEWORK-4.
 FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 102 111 BY SIMILARITY.
 FT NON_TER 111 111
 FT SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;
 SQ
 Query Match 66.0%; Score 384.5; DB 1; Length 111;
 Best Local Similarity 69.0%; Pred. No. 4.2e-34;
 Matches 78; Conservative 11; Mismatches 21; Indels 3; Gaps 2;
 QY 1 DIVVTGSPDLSAVLSGERVTMNCSSQSVLYSSNOKNYLAWYQKRGQSPKLLIYMASTR 60
 DB 1 DIVLTGSPASLAVSLGKATISCAQSDVYTG--BSYNMWYQKRGQSPKLLIYASNL 58
 QY 61 ESGVDPDFSGSGGSDTFTLTISVQAEADLAVVYCHQYLS-YFGGSKLEIK 112
 DB 59 ESGVPDRFTGSSGSDTFTLTINHPVEEDATYCHQSEDPWTGSGTLEIK 111

RT genes.";
 RL Can. J. Biochem. 58:176-187(1980).
 RN [3]
 RP MEDLINE=78186617; PubMed=418775;
 RA Smith G.P.;
 RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
 myeloma MPC 11.";
 RL Biochem. J. 171:337-347(1978).
 CC -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
 C-AMINO END, DUE TO A TANDEN DUPLICATION OF 36 NUCLEOTIDES AFTER THE
 CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
 RESIDUE OF TYPICAL KAPPA CHAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U00561; AAA8776.1; -
 DR PIR; A90823; KVM511.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal; Repeat.
 KW SIGNAL
 FT CHAIN 1 29 IG KAPPA CHAIN V-V REGION MPC11.
 FT DOMAIN 42 64 FRAMEWORK-1.
 FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 76 90 FRAMEWORK-2.
 FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 98 129 FRAMEWORK-3.
 FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 139 148 FRAMEWORK-4.
 FT REPEAT 26 35
 FT REPEAT 38 47
 FT NON TER 149
 SQ SEQUENCE 149 AA; 16434 MW; B0480C87B662AC3E CRC64;
 Query Match 65.1%; Score 379.5; DB 1; Length 149;
 Best Local Similarity 69.0%; Pred. No. 2e-33;
 Matches 78; Conservative 12; Mismatches 16; Indels 7; Gaps 2;
 QY 1 DIVWTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAVYQCKPGSPKLLITYMASTR 60
 DB 42 DIVWTQSHKMTSVSGRVSITRKASQDV-----STTAVMYQCKPGSPKLLITYASVSR 95
 QY 61 ESGVPPDRFSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTKEIK 112
 DB 96 YTGVPDRFSTSGSGTDTFTLTSSVQAEADLAVYYCQGHYSPFPFGGTKEIK 148
 RESULT 12
 KV3B HUMAN STANDARD; PRT; 109 AA.
 ID KV3B HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region S1S.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=82046598; PubMed=6794615;
 RX MEDLINE=82046598; PubMed=6794615;

RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
 RT group.";
 RL Biochemistry 20:5816-5822(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01892; K3HUS1.
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON TER 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
 Query Match 64.7%; Score 377; DB 1; Length 109;
 Best Local Similarity 64.6%; Pred. No. 2.6e-33;
 Matches 73; Conservative 20; Mismatches 14; Indels 6; Gaps 2;
 QY 1 DIVWTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAVYQCKPGSPKLLITYMASTR 60
 DB 1 EIVLTQSGFTLSLSPGEATLSCASQSV-----SNSYLAVYQCKPGQAPRLLYGASSR 55
 QY 61 ESGVPPDRFSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTKEIK 112
 DB 56 ATGVPDRFSGSGGTDTFTLTSSVQAEADLAVYYCQGHYSPFPFGGTKEIK 108
 RESULT 13
 KV3D HUMAN STANDARD; PRT; 109 AA.
 ID KV3D HUMAN STANDARD; PRT; 109 AA.
 AC P01622;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region T1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=72186439; PubMed=5027703;
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 RT T1). IV. The complete amino acid sequence and its significance for
 RT the mechanism of antibody production.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A Bence-Jones protein.
 DR PIR; A01895; K3HUT1.
 DR HSSP; P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON TER 109
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDDC7749BC CRC64;

Query Match 64.5%; Score 376; DB 1; Length 109;
 Best Local Similarity 64.6%; Pred. No. 3.3e-33;
 Matches 73; Conservative 20; Mismatches 14; Indels 6; Gaps 2;

QY 1 DIVMTQSPSLAVSLGERVTNCKSSQSVLYSSNCKNYLAWYQKRGSGPKLLIYMASTR 60
 DB 1.EVLVTSPTLSLSPKRAITLSCRAQSV-----SNSFLAWYQKRGGAPELLIYVASSR 55
 QY 61 ESGVDPDFSGSGSGGTDFTLTITSSVQAEDLAVYVCHQYLS-SYTFGGGKTLEIK 112
 DB 56 ATGIPRFSGSGSGGTDFTLTITSLRLEPEDFAVYCCQYSSPSTFGGTIVELK 108

RESULT 14
 KVIA_MOUSE STANDARD; PRT; 114 AA.

AC P01632;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Ig kappa chain V-I region S107A.
 DB Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=81241357; PubMed=6788890;
 RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Schaff M.D.;
 RT "Nucleic acid and protein sequences of phosphocholine-binding light
 chain";
 RT J. Exp. Med. 153:1366-1370 (1981).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U29423; AAC00033.1; -
 DR PIR; A01915; KYMS7A.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG_Like; 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 103 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 104 113 FRAMEWORK-4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON TER 114
 SQ SEQUENCE 114 AA; 12717 MW; 32008BCE9DBE67B CRC64;

Query Match 64.4%; Score 375.5; DB 1; Length 114;
 Best Local Similarity 69.3%; Pred. No. 4e-33;
 Matches 79; Conservative 12; Mismatches 20; Indels 3; Gaps 3;

QY 1 DIVMTQSPSLAVSLGERVTNCKSSQSVLYSSNCKNYLAWYQKRGSGPKLLIYMASTR 59
 DB 1 DIVMTQSPSLAVSLGERVTNCKSSQSVLYSSNCKNYLAWYQKRGSGPKLLIYMASTR 59
 QY 60 RESGVDPDFSGSGSGGTDFTLTITSSVQAEDLAVYVCHQYLS-SYTFGGGKTLEIK 112
 DB 60 RYIGVDPDFSGSGSGGTDFTLTITSSVQAEDLAVYVCHQYLS-SYTFGGGKTLEIK 113

RESULT 15

KVIM_HUMAN STANDARD; PRT; 108 AA.

AC P01603;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Ig kappa chain V-I region Iay.
 DB Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT IgM anti-gamma globulins (Iay/Pom) with shared idiotypic
 RT specificities";
 RT Scand. J. Immunol. 5:677-684 (1976).
 CC -----
 CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN PGM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.

DR PIR; A01871; KIHULY.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG_Like; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 64.2%; Score 374.5; DB 1; Length 108;
 Best Local Similarity 66.4%; Pred. No. 4.7e-33;
 Matches 75; Conservative 14; Mismatches 17; Indels 7; Gaps 2;

QY 1 DIVMTQSPSLAVSLGERVTNCKSSQSVLYSSNCKNYLAWYQKRGSGPKLLIYMASTR 60
 DB 1 DIVMTQSPSLAVSLGERVTNCKSSQSVLYSSNCKNYLAWYQKRGSGPKLLIYMASTR 54
 QY 61 ESGVDPDFSGSGSGGTDFTLTITSSVQAEDLAVYVCHQYLS-SYTFGGGKTLEIK 112
 DB 55 EAGVPSRFSGSGSGGTDFTLTITSSLOPEDIAIYCCQYNNMPPTFGGTIVELK 107

Search completed: March 26, 2004, 05:04:46
 Job time: 7.75177 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:13 / Search time 32.3688 Seconds

(without alignments)
1091.732 Million cell updates/sec

Title: US-10-056-052a-18

Perfect score: 583
Sequence: 1 DIVMQSPDGLAVSLGERTV.....YCHQYLSSYTRGGTKLEIK 112

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_proteus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	432.5	74.2	107	11 Q9ERZ9	Q9ERZ9 mus musculu
2	391	67.1	109	4 Q9UL78	Q9UL78 homo sapien
3	389	66.7	107	4 Q96SA9	Q96SA9 homo sapien
4	383	65.7	238	11 Q9NM37	Q9NM37 mus musculu
5	378.5	64.9	108	4 Q9UL70	Q9UL70 homo sapien
6	378	64.8	109	4 Q9UL85	Q9UL85 homo sapien
7	377	64.6	238	11 Q8VC16	Q8VC16 mus musculu
8	376.5	64.6	108	4 Q9UL77	Q9UL77 homo sapien
9	376.5	64.6	111	11 Q920E9	Q920E9 mus musculu
10	376	64.5	107	4 Q9UL81	Q9UL81 homo sapien
11	372.5	63.9	108	4 Q9UL83	Q9UL83 homo sapien
12	371.5	63.7	108	4 Q9UL79	Q9UL79 homo sapien
13	369	63.3	239	4 Q8NEK0	Q8NEK0 homo sapien
14	367	63.0	109	4 Q9UL86	Q9UL86 homo sapien
15	366	62.8	239	11 Q8VC55	Q8VC55 mus musculu
16	363.5	62.3	99	11 Q9UL74	Q9UL74 mus musculu

17	363.5	62.3	108	11 Q8VIC0	Q8VIC0 mus musculu
18	362	62.1	243	11 Q7TQM2	Q7TQM2 mus musculu
19	360.5	61.8	236	4 Q723Y4	Q723Y4 homo sapien
20	359	61.6	239	11 Q8X0F8	Q8X0F8 mus musculu
21	358.5	61.5	111	11 Q8LIU6	Q8LIU6 mus musculu
22	355.5	61.0	234	4 Q72473	Q72473 homo sapien
23	355.5	61.0	236	11 Q7TMR3	Q7TMR3 mus musculu
24	353.5	60.6	114	4 Q9UL80	Q9UL80 homo sapien
25	350	60.0	239	4 Q8TCD0	Q8TCD0 homo sapien
26	349	59.9	104	11 Q9JL82	Q9JL82 mus musculu
27	345.5	59.3	236	11 Q7TS98	Q7TS98 mus musculu
28	344.5	59.1	233	11 Q9IWS9	Q9IWS9 mus musculu
29	343	58.8	112	11 Q8KIF3	Q8KIF3 mus musculu
30	342.5	58.7	131	11 Q8IIC3	Q8IIC3 mus musculu
31	341.5	58.6	214	11 Q8RIAS	Q8RIAS mus musculu
32	341	58.5	114	11 Q8KIF1	Q8KIF1 mus musculu
33	336.5	57.7	237	13 Q7S236	Q7S236 xenopus lae
34	335.5	57.5	234	11 Q8R062	Q8R062 mus musculu
35	335.5	57.5	298	11 Q9QYF0	Q9QYF0 mus musculu
36	333.5	57.2	109	11 Q920E6	Q920E6 mus musculu
37	333	57.1	134	11 Q8YDD0	Q8YDD0 mus musculu
38	333	57.1	235	11 Q7TMR0	Q7TMR0 mus musculu
39	321.5	55.1	103	11 Q9JL80	Q9JL80 mus musculu
40	320.5	55.0	107	11 Q9JL84	Q9JL84 mus musculu
41	320.5	55.0	116	4 Q96P66	Q96P66 homo sapien
42	320.5	55.0	234	11 Q9IWF8	Q9IWF8 mus musculu
43	319	54.7	112	11 Q8KIF2	Q8KIF2 mus musculu
44	315.5	54.1	101	11 Q9JL78	Q9JL78 mus musculu
45	313	53.7	106	5 Q9U410	Q9U410 schistosoma

ALIGNMENTS

RESULT 1
Q9ERZ9 PRELIMINARY; PRT; 107 AA.

AC Q9ERZ9; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Anti human TNF-alpha light chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]
SEQUENCE FROM N.A.

RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

RT "Cloning and sequencing of the light chain fragment of variable region

RT genes of an anti-hTNF-a monoclonal antibody.";

RL J. Cell. Mol. Immunol. 12:21-26(1996).

RN [2]
SEQUENCE FROM N.A.

RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

RT "Construction and sequencing of the single-chain antibody gene of a

RT human TNF-alpha specific monoclonal antibody.";

RL Ti 4 Chun I Ya Hsien Hsien Pao 15:373-376(1998).

RN [3]
SEQUENCE FROM N.A.

RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;

RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AF262753; AAC33804.1; -

DR PDB: 2AP2; 24-NOV-99.

DR PDB: 45C9; 24-JUL-02.

DR PDB: 45CA; 24-JUL-02.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG_1.

DR SMART; SMO0406; IGV_1.

DR PROSITE; PS00835; IG-LIKE; 1.

FT NON TER 107

FT SEQUENCE 107 AA; 11784 MW; 2B15EPA604A26C3 CRC64;

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Query Match      74.2%; Score 432.5; DB 11; Length 107;
Best Local Similarity 77.6%; Pred. No. 1.1e-39;
Matches 83; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

QY 4 MTQSPDLSAVLSGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYWASTREG 63
DB 1 MTQSPDLSAVSQKTYMCKSSQSVLYNSNTQKNYLAWYQKPGQSPKLLIYFASRREG 60

QY 64 VPRFSGSGGSDFTLTISVQAEADLAVYYCHQ-VLSTTFGGGTCL 109
DB 61 VPRFSGSGGSDFTLTISVQAEADLAVYYCHQVPRFSGGTCL 107

RESULT 2
Q9UTL78 PRELIMINARY; PRT; 109 AA.
ID Q9UTL78
AC Q9UTL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.
DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSSP: P80362; IWTL.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SMO0406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52ECTBE197 CRC64;

Query Match      67.1%; Score 391; DB 4; Length 109;
Best Local Similarity 67.3%; Pred. No. 4e-35;
Matches 76; Conservative 18; Mismatches 13; Indels 6; Gaps 2;

QY 1 DIWVTQSPDLSAVLSGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYWASTR 60
DB 1 EIVLTQSPGTLSPGSRATLSCRASGV-----SSSYLAWYQKPGQAPRLLIYGASST 55

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QY 61 ESGVPRFSGSGGSDFTLTISVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112
DB 56 ATGIPDRFSGSGGSDFTLTISLPEPDCAVYICQYQSSPLTFGGGTVEIK 108

RESULT 3
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RX MEDLINE=98375893; PubMed=9712075;
RA Addison E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL: U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SMO0406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match      66.7%; Score 389; DB 4; Length 107;
Best Local Similarity 67.0%; Pred. No. 6.e-35;
Matches 75; Conservative 15; Mismatches 16; Indels 6; Gaps 1;

QY 1 DIWVTQSPDLSAVLSGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYWASTR 60
DB 1 DIWVTQSPDLSAVSGDVTITCRASQSI-----SSYLMYQKPGKAPKLLIYAASTL 54

QY 61 ESGVPRFSGSGGSDFTLTISVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112
DB 55 QSGVPRFSGSGGSDFTLTISLQPEDFATYYCQGSYSLTFGGGTVEIK 106

RESULT 4
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RX MEDLINE=98375893; PubMed=9712075;
RA Strassberg R.;
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002035; AA02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.

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DR PIR; C32248; C32248.
 DR PIR; F32530; F32530.
 DR PIR; PH1042; PH1042.
 DR PIR; PH1043; PH1043.
 DR PIR; PH1044; PH1044.
 DR PIR; S07455; S07455.
 DR PIR; S16112; S16112.
 DR PIR; S24500; S24500.
 DR PIR; S24501; S24501.
 DR PIR; S24503; S24503.
 DR PIR; S24504; S24504.
 DR PIR; S24529; S24529.
 DR PIR; S24532; S24532.
 DR PIR; S24533; S24533.
 DR PIR; S24535; S24535.
 DR PIR; S24536; S24536.
 DR PIR; S24538; S24538.
 DR PDB; 1191; 25-DEC-02.
 DR PDB; 1102; 31-JUL-02.
 DR PDB; 1104; 31-JUL-02.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06408801330A CRC64;

Query Match 65.7%; Score 383; DB 11; Length 238;
 Best Local Similarity 69.0%; Pred. No. 8.3e-34;
 Matches 78; Conservative 12; Mismatches 21; Indels 2; Gaps 2;

QY 1 DIVMTQSPDLSAVSGERVTMCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
 DB 20 DVTMTQTPSLPVSIGDQASISCRSSQSVLH-SNNTLYEWYLQKPGQSPKLLIYKVENR 78
 QY 61 ESGVPPDFSGSGGTDFTLTISISVQAEDLAVYYCHQYLS--SYFGGGLTLEIK 112
 DB 79 FSGVPPDFSGSGGTDFTLTISIRVEDLVGYVYCCGSGHVPPTFGSGTLEIK 131

RESULT 5
 Q9UL70 PRELIMINARY; PRT; 108 AA.
 ID Q9UL70;
 AC Q9UL70;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035044; AAD56280.1; -.
 DR PIR; PH0863; PH0863.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1

FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
 Query Match 64.9%; Score 378.5; DB 4; Length 108;
 Best Local Similarity 67.3%; Pred. No. 9.3e-34;
 Matches 76; Conservative 13; Mismatches 17; Indels 7; Gaps 2;

QY 1 DIVMTQSPDLSAVSGERVTMCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
 DB 1 DIVMTQSPDLSAVSGDRITTCRASQGI-----SNILAWYQKPGKPKSLIYAASLT 54
 QY 61 ESGVPPDFSGSGGTDFTLTISISVQAEDLAVYYCHQYLS--YTFGGGLTLEIK 112
 DB 55 QSGVPPDFSGSGGTDFTLTISLQPEDVATVYCCQKNSAPRTFGSGTLEIK 107

RESULT 6
 Q9UL85 PRELIMINARY; PRT; 109 AA.
 ID Q9UL85;
 AC Q9UL85;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035029; AAD56265.1; -.
 DR PIR; D30609; D30609.
 DR HSSP; P80362; IWTI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 109
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 64.8%; Score 378; DB 4; Length 109;
 Best Local Similarity 67.5%; Pred. No. 1.1e-33;
 Matches 77; Conservative 17; Mismatches 12; Indels 8; Gaps 3;

QY 1 DIVMTQSPDLSAVSGERVTMCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
 DB 1 DIVMTQSPDLSAVSGERATLSCWASQSI--SSN---LAWYQKPGQAPRLIYGASTR 54
 QY 61 ESGVPPDFSGSGGTDFTLTISISVQAEDLAVYYCHQYLS--SYFGGGLTLEIK 112
 DB 55 ATGIPARPSGSGGTDFTLTISLSQSDPAIHCOQYNPNPPLTFGGTIVEIK 108
 RESULT 7
 Q9VC16 PRELIMINARY; PRT; 238 AA.
 ID Q9VC16;
 AC Q9VC16;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCB1_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019760; AAI19760.1; -.
DR PIR: A27887; A27887.
DR PIR: A32448; A32448.
DR PIR: A33933; A33933.
DR PIR: B27887; B27887.
DR PIR: B30577; B30577.
DR PIR: B31485; B31485.
DR PIR: B32248; B32248.
DR PIR: B41940; B41940.
DR PIR: C27887; C27887.
DR PIR: C32248; C32248.
DR PIR: C34904; C34904.
DR PIR: D27887; D27887.
DR PIR: D29380; D29380.
DR PIR: E28833; E28833.
DR PIR: F32530; F32530.
DR PIR: H31485; H31485.
DR PIR: PH0106; PH0106.
DR PIR: PH1030; PH1030.
DR PIR: PH1031; PH1031.
DR PIR: PH1034; PH1034.
DR PIR: PLO257; PLO257.
DR PIR: PLO359; PLO359.
DR PIR: S07455; S07455.
DR PIR: S16112; S16112.
DR PIR: S26334; S26334.
DR PIR: S53750; S53750.
DR PIR: S60066; S60066.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414D CRC64;

Query Match 64.7%; Score 377; DB 11; Length 238;
Best Local Similarity 67.8%; Pred. No. 3.8e-33;
Matches 78; Conservative 15; Mismatches 16; Indels 6; Gaps 3;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNOKXYLAWYQKPGQSPKLLIYMASTR 60
DB 20 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNOKXYLAWYQKPGQSPKLLIYMASTR 78
QY 61 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSY--TFGGGTKLEIK 112
DB 79 FSGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSY--TFGGGTKLEIK 131

RESULT 8
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77;
AC Q9UL77;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RM MEDLINE=98277139; PubMed=9614934;
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RA Wu X., Jau B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035037; AAD56273.1; -.
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR HSSP: P01607; IREI.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 64.6%; Score 376.5; DB 4; Length 108;
Best Local Similarity 65.5%; Pred. No. 1.5e-33;
Matches 74; Conservative 16; Mismatches 16; Indels 7; Gaps 2;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNOKXYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNOKXYLAWYQKPGQSPKLLIYMASTR 54
QY 61 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTKLEIK 112
DB 55 QSGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTKLEIK 107

RESULT 9
Q920E9 PRELIMINARY; PRT; 111 AA.
ID Q920E9;
AC Q920E9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Jape A., Jennings I.G., Horatis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307935; AAL09419.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA685826 CRC64;
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Query Match 64.6%; Score 376.5; DB 11; Length 111;
Best Local Similarity 68.1%; Pred. No. 1.6e-33;
Matches 77; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNOKXYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNOKXYLAWYQKPGQSPKLLIYMASTR 58
QY 61 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTKLEIK 112
DB 59 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTKLEIK 111
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RESULT 10
Q9UL81      PRELIMINARY;      PRT;      107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.,
  "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus."
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.1.
DR SMART; SMO0406; Ig_v.1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 64.3%; Score 376; DB 4; Length 107;
Matches 72; Conservative 16; Mismatches 18; Indels 6; Gaps 1;

QY 1 DIWVTQSPSLAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIWVTQSPSLAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 60
QY 55 QSGVPSRFSGSGSGTDFLTITSSVQAEADLAIVYCHQYLS-SYTFGGGTGLEIK 112
DB 55 QSGVPSRFSGSGSGTDFLTITSSVQAEADLAIVYCHQYLS-SYTFGGGTGLEIK 106

RESULT 11
Q9UL83      PRELIMINARY;      PRT;      108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.,
  "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus."
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; IWTL.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.1.
DR SMART; SMO0406; Ig_v.1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match
Best Local Similarity 67.3%; Score 371.5; DB 4; Length 108;
Matches 76; Conservative 17; Mismatches 13; Indels 7; Gaps 3;

QY 1 DIWVTQSPSLAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIWVTQSPSLAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 54
QY 61 ESGVPSRFSGSGSGTDFLTITSSVQAEADLAIVYCHQYLS-SYTFGGGTGLEIK 112
DB 55 ATGIPARFSGSGSGTDFLTITSSVQAEADLAIVYCHQYLS-SYTFGGGTGLEIK 107

RESULT 12
Q9UL79      PRELIMINARY;      PRT;      108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.,
  "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus."
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.1.
DR SMART; SMO0406; Ig_v.1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match
Best Local Similarity 65.5%; Score 371.5; DB 4; Length 108;
Matches 74; Conservative 14; Mismatches 18; Indels 7; Gaps 2;

QY 1 DIWVTQSPSLAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIWVTQSPSLAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 54
QY 61 ESGVPSRFSGSGSGTDFLTITSSVQAEADLAIVYCHQYLS-SYTFGGGTGLEIK 112
DB 55 QSGVPSRFSGSGSGTDFLTITSSVQAEADLAIVYCHQYLS-SYTFGGGTGLEIK 107

RESULT 13
Q9NEK0      PRELIMINARY;      PRT;      239 AA.
AC Q9NEK0;
DT 01-OCT-2002 (TREMBlrel. 22, Created)

```

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030814; AAH30814.1; -
 DR PIR; S23638; S23638.
 DR PIR; S34091; S34091.
 DR PIR; S40357; S40357.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003606; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00407; IgC1.1.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; FSE20AD3B0552C0A CRC64;

 Query Match 63.3%; Score 369; DB 4; Length 239;
 Best Local Similarity 67.3%; Pred. No. 2.9e-32;
 Matches 76; Conservative 13; Mismatches 22; Indels 2; Gaps 2;

 QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNCKNYLAWYQKPGQSPKLLIYMASTR 60
 DB 21 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNCKNYLAWYQKPGQSPKLLIYMASTR 79
 QY 61 ESGVPRDFSSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTGLEIK 112
 DB 80 ASGVPRDFSSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTGLEIK 132

 RESULT 14
 Q9UL86 PRELIMINARY; PRT; 109 AA.
 AC Q9UL86;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035028; AAD56264.1; -
 DR PIR; B30607; B30607.
 DR PIR; I30601; I30601.
 DR HSSP; P80362; 1MTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 1 109 109
 FT

SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACA83 CRC64;

 Query Match 63.0%; Score 367; DB 4; Length 109;
 Best Local Similarity 62.8%; Pred. No. 1.7e-32;
 Matches 71; Conservative 20; Mismatches 16; Indels 6; Gaps 2;

 QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNCKNYLAWYQKPGQSPKLLIYMASTR 60
 DB 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNCKNYLAWYQKPGQSPKLLIYMASTR 55
 QY 61 ESGVPRDFSSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTGLEIK 112
 DB 56 ATGIPDRFSSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTGLEIK 108

 RESULT 15
 Q8VC55 PRELIMINARY; PRT; 239 AA.
 AC Q8VC55;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021781; AAH21781.1; -
 DR PIR; A33933; A33933.
 DR PIR; A33933; A33933.
 DR PIR; A33933; A33933.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR004214; Conotoxin.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF02950; Conotoxin; 1.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; IGV.1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

 Query Match 62.8%; Score 366; DB 11; Length 239;
 Best Local Similarity 65.8%; Pred. No. 6.2e-32;
 Matches 75; Conservative 18; Mismatches 17; Indels 4; Gaps 3;

 QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNCKNYLAWYQKPGQSPKLLIYMASTR 60
 DB 21 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNCKNYLAWYQKPGQSPKLLIYMASTR 79
 QY 61 ESGVPRDFSSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTGLEIK 112
 DB 80 FSGVPRDFSSGSGGTDTFTLTSSVQAEADLAVYYCHQYLSS-YTFGGGTGLEIK 132

Search completed: March 26, 2004, 05:07:46
 Job time : 35.3688 secs

XX The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing *S. aureus*
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus ClfA protein, S. aureus ClfA3 protein, or the S. aureus N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is staphylococcus aureus ClfA specific monoclonal
 CC antibody 12-9VH-Hu (humanised variable light sequence) protein

SO Sequence 121 AA;

Query Match 100.0%; Score 647; DB 5; Length 121;
 Best Local Similarity 100.0%; Pred. No. 7,6e-53;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLSTITCTISGFSLSRYSVHWRQPPGKGLKLEMLGIMGGNTDYN 60
 DB 1 QVQLKESGPGLVKPSQTLSTITCTISGFSLSRYSVHWRQPPGKGLKLEMLGIMGGNTDYN 60
 QY 61 SALKSRISISKDKNKQVFLKNSLTADTAVYVCARKGEFFYGYDGFYVWGQGLTVTVS 120
 DB 61 SALKSRISISKDKNKQVFLKNSLTADTAVYVCARKGEFFYGYDGFYVWGQGLTVTVS 120
 QY 121 S 121
 DB 121 S 121

RESULT 2

AAE29267 standard; protein; 121 AA.

AAE29267;

27-JAN-2003 (first entry)

S. aureus ClfA specific monoclonal antibody 12-9VHC-1 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; ClfA40; ClfA3; N3 protein;
 KM immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX Key Location/Qualifiers
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..65
 FT /note= "CDR2"
 FT Region 98..110
 FT /note= "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.

XX 12-MAR-2001; 2001US-0274611P.

XX 18-JUN-2001; 2001US-0298413P.

XX 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

XX Pateti JM, Hutchins JT, Domanski P, Patel P, Hall A;
 XX WPI; 2002-759834/82.
 XX N-PSDB; AAD46866.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
 PT treating or preventing *Staphylococcus aureus* infection e.g. wound
 PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
 PT a human or animal.

XX Claim 13; Page 36; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing *S. aureus*
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus ClfA protein, S. aureus ClfA3 protein, or the S. aureus N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is staphylococcus aureus ClfA specific monoclonal
 CC antibody 12-9VHC-1 (variable heavy sequence) protein

SO Sequence 121 AA;

Query Match 93.5%; Score 605; DB 5; Length 121;
 Best Local Similarity 92.6%; Pred. No. 6,5e-49;
 Matches 112; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLSTITCTISGFSLSRYSVHWRQPPGKGLKLEMLGIMGGNTDYN 60
 DB 1 QVQLKESGPGLVKPSQTLSTITCTISGFSLSRYSVHWRQPPGKGLKLEMLGIMGGNTDYN 60
 QY 61 SALKSRISISKDKNKQVFLKNSLTADTAVYVCARKGEFFYGYDGFYVWGQGLTVTVS 120
 DB 61 SALKSRISISKDKNKQVFLKNSLTADTAVYVCARKGEFFYGYDGFYVWGQGLTVTVS 120
 QY 121 S 121
 DB 121 A 121

RESULT 3

AAE29269 standard; protein; 118 AA.

AAE29269;

27-JAN-2003 (first entry)

S. aureus ClfA specific monoclonal antibody 35-220VHC-1 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; ClfA40; ClfA3; N3 protein;
 KM immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX Key Location/Qualifiers
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 50..65
 FT /note= "CDR2"
 FT Region 98..107
 FT /note= "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.

XX 12-MAR-2001; 2001US-0274611P.

XX 18-JUN-2001; 2001US-0298413P.

XX 30-JUL-2001; 2001US-0308116P.

XX 30-SEP-1999; 99UP-00278290.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266163/27.
 XX
 XX Human type complementation-determining domain transplanted antibody and
 XX derivatives against ganglioside GD2, useful in diagnosis and therapy of
 XX e.g. tumors, has low antigenicity, little side effects but potent
 XX activity in cancer.
 XX
 XX Claim 10; Page 102-103; 123pp; Japanese.
 XX
 XX The present invention describes an antibody, which can react specifically
 XX with ganglioside GD2, and is transplanted with a human type
 XX complementation-determining domain (CDR), or its fragments. The antibody
 XX and its derivatives are useful in diagnosis and therapy of tumours,
 XX particularly cancer diagnosis. The present sequence is a protein used in
 XX the exemplification of the invention
 XX
 XX Sequence 118 AA;
 XX
 XX Query Match 80.9%; Score 523.5; DB 4; Length 118;
 XX Best Local Similarity 80.2%; Pred. No. 2.6e-41;
 XX Matches 97; Conservative 13; Mismatches 8; Indels 3; Gaps 1;
 XX
 QY 1 QVQLKESGPGGLVPSQSLTCTISGFSLSRYGVHWVROPKGLKGLMIGMGNTDYN 60
 DB 1 QVQLQESGPGGLVPSQSLTCTISGFSLSYNIHWVROPKGLKGLMIGMGNTDYN 60
 QY 61 SALKSRISISKDMSKNOVFLKMSLTADPAVYVYCARKEFFYYGYDGFYWGGLTVTS 120
 DB 61 SALKMSRLTISKDMSKNOVFLKMSLTADPAVYVYCARKEFFYYGYDGFYWGGLTVTS 117
 QY 121 S 121
 DB 118 S 118
 XX
 XX RESULT 6
 XX AAB81972
 XX ID AAB81972 standard; proein; 581 AA.
 XX
 XX AAB81972;
 XX
 XX 03-JUL-2001 (first entry)
 XX
 XX Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
 XX
 XX Ganglioside; GD2; complementation determining region; CDR; antibody;
 XX mouse; cancer.
 XX
 XX Synthetic.
 XX
 XX WO200123573-A1.
 XX
 XX 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000WO-JP006773.
 XX
 XX 30-SEP-1999; 99JP-00278290.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 XX WPI; 2001-266163/27.
 XX
 XX Human type complementation-determining domain transplanted antibody and
 XX derivatives against ganglioside GD2, useful in diagnosis and therapy of

PT e.g. tumors, has low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 XX Example 3; Page 111-114; 123pp; Japanese.
 XX
 XX The present invention describes an antibody, which can react specifically
 XX with ganglioside GD2, and is transplanted with a human type
 XX complementation-determining domain (CDR), or its fragments. The antibody
 XX and its derivatives are useful in diagnosis and therapy of tumours,
 XX particularly cancer diagnosis. The present sequence is a protein used in
 XX the exemplification of the invention
 XX
 XX Sequence 581 AA;
 XX
 XX Query Match 80.9%; Score 523.5; DB 4; Length 581;
 XX Best Local Similarity 80.2%; Pred. No. 1.6e-40;
 XX Matches 97; Conservative 13; Mismatches 8; Indels 3; Gaps 1;
 XX
 QY 1 QVQLKESGPGGLVPSQSLTCTISGFSLSRYGVHWVROPKGLKGLMIGMGNTDYN 60
 DB 1 QVQLQESGPGGLVPSQSLTCTISGFSLSYNIHWVROPKGLKGLMIGMGNTDYN 60
 QY 61 SALKSRISISKDMSKNOVFLKMSLTADPAVYVYCARKEFFYYGYDGFYWGGLTVTS 120
 DB 61 SALKMSRLTISKDMSKNOVFLKMSLTADPAVYVYCARKEFFYYGYDGFYWGGLTVTS 117
 QY 121 S 121
 DB 118 S 118
 XX
 XX RESULT 7
 XX ABO18564
 XX ID ABO18564 standard; proein; 118 AA.
 XX
 XX ABO18564;
 XX
 XX 18-FEB-2003 (first entry)
 XX
 XX Ganglioside-associated recombinant antibody related VH3 P3 protein.
 XX
 XX Cytostatic; chimeric antibody; monoclonal antibody; ECAC 94113026;
 XX N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
 XX breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
 XX sarcoma; neuroectodermal.
 XX
 XX Unidentified.
 XX
 XX WO200281496-A2.
 XX
 XX 17-OCT-2002.
 XX
 XX 08-APR-2002; 2002WO-CU000003.
 XX
 XX 06-APR-2001; 2001CU-00000084.
 XX
 XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 XX (IDRI/) MATEO DE ACOSTA DEL RIO C M.
 XX (VALL/) LOMBARDEO VALLADARES J.
 XX (NAVA/) ROQUE NAVARRO L T.
 XX (REQU/) LOPEZ REQUENA A.
 XX
 XX Mateo De Acosta Del Rio CM, Lombardero Valladares J;
 XX Roque Navarro LT, Lopez Requena A;
 XX N-PSDB; ABTI4038.
 XX
 XX WPI; 2003-046857/04.
 XX
 XX New chimeric antibodies, useful for treatment, prevention and diagnosis
 XX of tumors that express gangliosides, are derived from monoclonal
 XX antibodies P3 or 1E10.
 XX
 XX Example 6; Fig 1; 31pp; Spanish.

XX The invention relates to a chimeric antibody, derived from a monoclonal
CC antibody, which recognises N-glycosylated gangliosides and is produced by
CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
CC derived from the anti-idiotypic monoclonal 1E10 (recognising F3) are used
CC for treatment, localisation and in vivo identification of breast cancer
CC and melanoma, their metastases and relapses, tumours of lung, digestive
CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
CC This sequence represents a protein relating to the chimeric antibody of
CC the invention
CC
CC
SQ Sequence 118 AA;
Query Match 78.9%; Score 510.5; DB 6; Length 118;
Best Local Similarity 81.1%; Pred. No. 4.3e-40;
Matches 99; Conservative 6; Mismatches 8; Indels 9; Gaps 2;
QY 1 QVQLKESGPGLVPSQTLISITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGSGNTDYN 60
DB 1 QVQLKESGPGLVAPSQSLISITCTVSGFSLRSYVHWVRQPPGKLEWLGIMWGSGTIDYN 60
QY 61 SALKSRSLSTSKDSSKNQVFLKNNSLTAADTAVYYCARKEGFYYGDS-----FVYWGQGT 115
DB 61 SALKSRSLSTSKDSSKNQVFLKNNSLCTDDTAMYYCARSGV-----REGRAQAMFPAWGQGT 116
QY 116 LV 117
DB 117 LV 118
RESULT 8
AAB69675
ID AAB69675 standard; protein; 119 AA.
XX
XX AAB69675;
XX
XX 30-APR-2001 (first entry)
XX
XX Murine m1k-beta1 antibody heavy chain SEQ ID NO: 60.
XX
XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
XX light chain; graft versus host disease; transplant; autoimmune disease;
XX multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
XX Mus sp.
XX
XX OS
XX US6180370-B1.
XX
XX 30-JAN-2001.
XX
XX 07-JUN-1995; 95US-00484537.
XX
XX 28-DEC-1988; 88US-00290975.
XX
XX 13-FEB-1989; 89US-00310252.
XX
XX 28-SEP-1990; 90US-00590274.
XX
XX 19-DEC-1990; 90US-00634278.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Queen CL, Selick HE;
XX
XX WPI; 2001-190856/19.
XX
XX Producing humanized immunoglobulin, involves producing a cell containing
XX DNA segments encoding humanized heavy and light chain variable regions,
XX and expressing the DNA segments in the cell.
XX
XX Disclosure; Fig 5; 145pp; English.
XX
XX The present invention describes a method of producing humanised
XX immunoglobulins involving expressing in a cell a nucleic acid encoding a
XX humanised version of an immunoglobulin. This is obtained by comparing a

CC donor and human immunoglobulin and producing a combined antibody which
CC contains part of each. These are useful in the treatment of graft-versus-
CC host disease, transplant rejection, autoimmune diseases such as diabetes,
CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic
CC lupus erythematosus, herpes infections, CMV virus infections and myeloid
CC leukaemia. The present sequence is an antibody used to demonstrate the
CC method of the invention
CC
CC
SQ Sequence 119 AA;
Query Match 78.2%; Score 506; DB 4; Length 119;
Best Local Similarity 75.2%; Pred. No. 1.2e-39;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;
QY 1 QVQLKESGPGLVPSQTLISITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGSGNTDYN 60
DB 1 QVQLKESGPGLVAPSQSLISITCTVSGFVTSYGVHWIRQSPGKLEWLGIVMSGSTIDYN 60
QY 61 SALKSRSLSTSKDSSKNQVFLKNNSLTAADTAVYYCARKEGFYYGDSFYWGQGTIVTS 120
DB 61 AAFISRLTSTSKDSSKNQVFLKNNSLPADTAVYYCARAGD--YNYDGFAYWGQGTIVTS 118
QY 121 S 121
DB 119 A 119
RESULT 9
AAB69656
ID AAB69656 standard; protein; 138 AA.
XX
XX AAB69656;
XX
XX 30-APR-2001 (first entry)
XX
XX Murine m1k-beta1 antibody heavy chain SEQ ID NO: 33.
XX
XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
XX light chain; graft versus host disease; transplant; autoimmune disease;
XX multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
XX Mus sp.
XX
XX OS
XX US6180370-B1.
XX
XX 30-JAN-2001.
XX
XX 07-JUN-1995; 95US-00484537.
XX
XX 28-DEC-1988; 88US-00290975.
XX
XX 13-FEB-1989; 89US-00310252.
XX
XX 28-SEP-1990; 90US-00590274.
XX
XX 19-DEC-1990; 90US-00634278.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Queen CL, Selick HE;
XX
XX WPI; 2001-190856/19.
XX
XX N-PSDB; AAF58728.
XX
XX Producing humanized immunoglobulin, involves producing a cell containing
XX DNA segments encoding humanized heavy and light chain variable regions,
XX and expressing the DNA segments in the cell.
XX
XX Example 5; Fig 23; 145pp; English.
XX
XX The present invention describes a method of producing humanised
XX immunoglobulins involving expressing in a cell a nucleic acid encoding a
XX humanised version of an immunoglobulin. This is obtained by comparing a
XX donor and human immunoglobulin and producing a combined antibody which
XX contains part of each. These are useful in the treatment of graft-versus-

CC host disease, transplant rejection, autoimmune diseases such as diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic
 CC lupus erythematosus, herpes infections, CMV virus infections and myeloid
 CC leukaemia. The present sequence is an antibody used to demonstrate the
 CC method of the invention

XX Sequence 138 AA;

Query Match 78.2%; Score 506; DB 4; Length 138;
 Best Local Similarity 75.2%; Pred. No. 1.4e-39;

Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 OVQLKESGPGVLVPSQGLTSTICTGFSLSRYSVHWVRQPPGKLEWLGMIWGSGNTDYN 60
 DB 20 OVQLKESGPGVLVPSQGLTSTICTGFSLSRYSVHWVRQPPGKLEWLGMIWGSGNTDYN 79
 QY 61 SALKSRSLSTKDNKSNQVFLKKNLSLTADTAVYCARKEGFYVGDGFVYWGQTLVTVS 120
 DB 80 AAFIRLRLTISKDNKSNQVFLKKNLSLTADTAVYCARKEGFYVGDGFVYWGQTLVTVS 137
 QY 121 S 121
 DB 138 A 138

RESULT 10

AAE29298
 ID AAE29298 standard; protein; 115 AA.

AC AAE29298;

DT 27-JAN-2003 (first entry)

DE S. aureus ClfA specific monoclonal antibody 35-006VHC-1 protein.

KM Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
 KM immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
 KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

OS Staphylococcus aureus.

FT Key Location/Qualifiers
 FT Region 31..35

FT Region /note= "CDR1"
 FT Region 50..65
 FT Region /note= "CDR2"
 FT Region 98..104
 FT Region /note= "CDR3"

FN WO200272600-A2.

PD 19-SEP-2002.

PF 28-JAN-2002; 2002WO-US002296.

PR 26-JAN-2001; 2001US-0264072P.

PR 12-MAR-2001; 2001US-0274611P.

PR 18-JUN-2001; 2001US-0298413P.

PR 30-JUL-2001; 2001US-0308116P.

PA (INH1-) INHIBITEX INC.

PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

DR WPI; 2002-759834/82.

DR N-PSDB; AAD46964.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
 PT treating or preventing Staphylococcus aureus infection e.g. wound
 PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
 PT a human or animal.
 XX Example 7; Page 39; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing S. aureus
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is Staphylococcus aureus ClfA specific monoclonal
 CC antibody 35-006VHC-1 (variable heavy sequence) protein

XX Sequence 115 AA;

Query Match 78.1%; Score 505; DB 5; Length 115;
 Best Local Similarity 81.0%; Pred. No. 1.4e-39;

Matches 98; Conservative 8; Mismatches 9; Indels 6; Gaps 2;

QY 1 OVQLKESGPGVLVPSQGLTSTICTGFSLSRYSVHWVRQPPGKLEWLGMIWGSGNTDYN 60
 DB 1 OVQLKESGPGVLVPSQGLTSTICTGFSLSRYSVHWVRQPPGKLEWLGMIWGSGNTDYN 60
 QY 61 SALKSRSLSTKDNKSNQVFLKKNLSLTADTAVYCARKEGFYVGDGFVYWGQTLVTVS 120
 DB 61 SALKSRSLSTKDNKSNQVFLKKNLSLTADTAVYCARKEGFYVGDGFVYWGQTLVTVS 114
 QY 121 S 121
 DB 115 S 115

RESULT 11

AAW23025
 ID AAW23025 standard; protein; 113 AA.

AC AAW23025;

DT 17-OCT-2003 (revised)

DT 23-MAR-1998 (first entry)

DE Humanized 5D12 monoclonal antibody heavy chain variable region.

KM Human; B7 antigen; CD40; monoclonal antibody; B cell; growth;
 KM differentiation; allergy; autoimmune disease.

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

FN WO9711025-A1.

PD 28-AUG-1997.

PF 21-FEB-1997; 97WO-US002858.

PR 23-FEB-1996; 96US-00606293.

PA (CHIR) CHIRON CORP.

PI De Boer M;

DR WPI; 1997-435094/40.

DR N-PSDB; AAT79192.

XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
 PT prevent their growth and differentiation, useful to treat or prevent
 PT antibody mediated allergies and autoimmune diseases.
 XX Example 8; Fig 12; 64pp; English.

CC A novel humanised monoclonal antibody (MAb) has been developed which: (a)
 CC binds a human CD40 antigen on the surface of a B cell, to prevent its

CC growth and differentiation; and (b) has an effective number of exposed
 CC amino acids in its framework regions that are consistent with amino acid
 CC residues found in the corresponding framework regions of a human Ab to
 CC provide a reduced immunogenicity in humans. The present sequence
 CC represents humanized 5D12 monoclonal antibody heavy chain variable
 CC region, used in an example of the present invention. The Mab can be used
 CC to prevent or treat antibody mediated diseases, particularly
 CC immunoglobulin E (IGE) mediated allergies, systemic lupus erythematosus,
 CC primary biliary cirrhosis, idiopathic thrombocytopenia purpura and
 CC rheumatoid arthritis. The Mab inhibits the normal B cell response to CD40
 CC ligands at relatively low concentrations and is unlikely to cause any
 CC immune response in humans. (Updated on 17-OCT-2003 to standardise OS
 CC field)

XX
 SQ Sequence 113 AA;

Query March 77.6%; Score 502; DB 2; Length 113;
 Best Local Similarity 81.0%; Pred. No. 2.5e-33;
 Matches 98; Conservative 7; Mismatches 8; Indels 8; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWLGIMWGSGNTDY 60
 DB 1 QVQLVDSGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWLGIMWGSGNTDY 60
 QY 61 SALKSRSLISKDNSKNQVFLKXNSLTADTAVYYCARKGEFYGYDGFVYWGQGLVTYS 120
 DB 61 SALKSRSLISKDNSKNQVFLKXNSLTADTAVYYCARKGEFYGYDGFVYWGQGLVTYS 112
 QY 121 S 121
 DB 113 S 113

RESULT 12
 ID AAB10020 standard; protein; 121 AA.
 XX AAB10020;
 AC AAB10020;
 DT 01-NOV-2000 (first entry)
 XX
 DE H. pylori HSP60-binding antibody heavy chain protein.
 XX
 KM Acid-resistant microorganism; detection; faecal; intestine; infection;
 KM monoclonal antibody; heat shock protein; HSP60; heavy chain.
 XX
 OS Unidentified.
 XX
 PN WO200026671-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 29-OCT-1999; 99WO-EP008212.
 XX
 PR 29-OCT-1998; 98EP-00120517.
 XX
 PR 06-NOV-1998; 98EP-00120687.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
 PI Ringeis A;
 DR WPI; 2000-365747/31.
 DR N-PSDB; AAA40200.
 XX
 XX WPI; 2000-365747/31.
 PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a fecal sample with two binding reagents for
 PT antigens that survive intestinal passage.
 PS Disclosure; Fig 2; 84pp; German.
 CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal

CC sample with at least two different monoclonal antibodies (Mab) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting
 CC formation of a complex (C) between (I) and the corresponding antigen
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure, or
 CC (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
 CC tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents the H. pylori heat shock protein, HSP60-binding
 CC antibody (DMS ACC2356) heavy chain which is used to illustrate the method
 CC of the invention

XX
 SQ Sequence 121 AA;

Query March 76.7%; Score 496; DB 3; Length 121;
 Best Local Similarity 79.7%; Pred. No. 1e-38;
 Matches 98; Conservative 8; Mismatches 13; Indels 4; Gaps 3;

QY 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWLGIMWGSGNTDY 59
 DB 1 QVQLVDSGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWLGIMWGSGNTDY 60
 QY 60 NSALKSRSLISKDNSKNQVFLKXNSLTADTAVYYCARK-GEFYGYDGFVYWGQGLVT 118
 DB 61 NSALKSRSLISKDNSKNQVFLKXNSLTADTAVYYCARK-GEFYGYDGFVYWGQGLVT 118
 QY 119 VSS 121
 DB 119 VSS 121

RESULT 13
 ID ABR44627 standard; protein; 125 AA.
 XX ABR44627;
 AC ABR44627;
 DT 25-JUL-2003 (first entry)
 XX
 DE Murine variable heavy chain amino acid sequence MuvH1B.
 XX
 KM Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
 KM prostate specific membrane antigen; antiproliferative; antiarthritic;
 KM dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
 KM epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
 XX
 OS Neoplastic disorder.
 XX
 OS Mus musculus.
 XX
 OS Synthetic.
 XX
 PN WO2003024388-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 30-MAY-2002; 2002WO-US017204.
 XX
 PR 20-SEP-2001; 2001US-0324100P.
 XX
 PR 08-MAR-2002; 2002US-0362612P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Bander N;
 DR WPI; 2003-313319/30.
 XX

PT Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.

PS Disclosure; Fig 12B; 225pp; English.

XX The present invention describes a method (M1) for ablating or killing an
 CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
 CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
 CC vascular endothelial cell proximate to the cell, with an antibody (or its
 CC antigen-binding fragment), which binds specifically to the extracellular
 CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
 CC antibodies have antiproliferative, antiproliferative, dermatological, cytostatic,
 CC antiinflammatory and antiallergic activities, and can be used in
 CC vaccines. M1 is useful for treating a skin disorder in a subject, by
 CC administering to the subject, an amount of an antibody which binds
 CC specifically to the extracellular domain of PSMA (the subject is a
 CC mammal, preferably human and is having, or at risk of, a skin disorder).
 CC The skin disorder is a dermal or an epidermal disorder, and is selected
 CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
 CC vulgaris, eruptive (glutinate) psoriasis, psoriatic erythroderma,
 CC generalised pustular psoriasis (Von Zumbusch), annular pustular,
 CC psoriasis, and localized pustular psoriasis), psoriatic arthritis,
 CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosea,
 CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
 CC ichthyosiform dermatosis, keratoderma, dermatosis, and prokeratosis,
 CC preferably psoriasis. M1 is useful for treating a skin disorder such as
 CC an inflammatory or neoplastic disorder of the epidermis or dermis.
 CC Preferably an epidermal precancerous or cancerous lesion. M1 is also
 CC useful to treat or prevent disorders involving aberrant activity of PSMA-
 CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
 CC and ABR44613 to ABR44733 represent sequences used in the exemplification
 CC of the present invention

XX Sequence 125 AA:

Query Match 76.7%; Score 496; DB 6; Length 125;

Best Local Similarity 77.6%; Pred. No. 1e-38; Mismatches 14; Indels 4; Gaps 3;

Matches 97; Conservative 10; Mismatches 14; Indels 4; Gaps 3;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVH--WVQAPGKGLWMLGMWGAGNTD 58
 Db 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVH--WVQAPGKGLWMLGMWGAGNTD 60
 QY 59 YNSALKSRSLISKDNSTKQVFLKNNSLTAADTAIVYICAR-KGEFYY-GYDGFYWGQGT 116
 Db 61 YNSALMSRLISKDNSTKQVFLKNNSLQTDLTAMYCARDRGRYYSGVYAMDMWGQGT 120
 QY 117 VTWSS 121
 Db 121 VTWSS 125

RESULT 14

AA849243 standard; protein; 476 AA.

AC AAB49243;

DT 15-MAR-2001 (first entry)

DE Chimeric 4H6 anti-DR4 antibody heavy chain protein.

XX Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;

KW autoimmune.

OS Homo sapiens.

XX Synthetic.

XX WO20007349-A1.

XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US014599.
 XX 28-MAY-1999; 99US-00322875.
 XX (GERTH) GENENTECH INC.

PI Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;

DR WPI; 2001-041145/05.

XX Novel anti-death receptor 4 antibodies useful for treating cancer and
 PT immune related disorders such as rheumatoid arthritis, Sjogren's
 PT syndrome, Grave's disease and diabetes mellitus.

XX Claim 16; Fig 18; 126pp; English.

XX The present invention relates to an anti-death receptor 4 (DR4) antibody.

CC The antibodies of the invention are useful for inducing apoptosis in
 CC mammalian cancer cells such as colon cancer cells and for treating an
 CC immune-related disease in a mammal such as arthritis and autoimmune
 CC disease

XX Sequence 476 AA:

Query Match 76.7%; Score 496; DB 4; Length 476;

Best Local Similarity 76.2%; Pred. No. 4.7e-38; Mismatches 14; Indels 6; Gaps 2;

Matches 96; Conservative 10; Mismatches 14; Indels 6; Gaps 2;

QY 2 VQLKESGPGLVKPSQTLSTCTISGFSLSRYSVH--WVQAPGKGLWMLGMWGAGNTD 61
 Db 21 VQLKESGPGLVKPSQTLSTCTISGFSLSRYSVH--WVQAPGKGLWMLGMWGAGNTD 80
 QY 62 ALKSRSLISKDNSTKQVFLKNNSLTAADTAIVYICAR-KGEFYY-GYDGFYWGQGT 115
 Db 81 ALMSRLISKDNSTKQVFLKNNSLQTDLTAMYCARDRGRYYSGVYAMDMWGQGT 140

QY 116 LTVSS 121

Db 141 LTVSS 146

RESULT 15

ABJ18566 standard; protein; 117 AA.

AC ABJ18566;

DT 18-FEB-2003 (first entry)

DE Ganglioside-associated recombinant antibody related VHP3 protein #2.

XX Cytostatic; chimeric antibody; monoclonal antibody; ECACC 9411026;

KW N-glycosylated ganglioside; anti-idiotypic monoclonal 1810; metastatic;

KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;

KW sarcoma; neuroectodermal.

XX Unidentified.

XX WO200281496-A2.

PD 17-OCT-2002.

XX 08-APR-2002; 2002WO-CU000003.

XX 06-APR-2001; 2001CU-00000084.

PA (IMMUNO-) CENT IMMUNOLOGICAL MOLECULAR.

PA (DRUG) MATER DE ACOSTA DEL RIO C M.

PA (NANA/) ROQUE NAVARRO L T.

XX (REQV/) LOPEZ REQUENA A.

PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
PI Roque Navarro LT, Lopez Requena A;
DR WPI; 2003-046857/04.

XX New chimeric antibodies, useful for treatment, prevention and diagnosis
PT of tumors that express gangliosides, are derived from monoclonal
PT antibodies P3 or 1E10.

XX Example 6; Fig 3; 31pp; Spanish.

CC The invention relates to a chimeric antibody, derived from a monoclonal
CC antibody, which recognises N-glycosylated gangliosides and is produced by
CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
CC derived from the anti-idiotypic monoclonal 1E10 (recognising P3) are used
CC for treatment, localisation and in vivo identification of breast cancer
CC and melanoma, their metastases and relapses, tumours of lung, digestive
CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
CC This sequence represents a protein relating to the chimeric antibody of
CC the invention

CC Sequence 117 AA;

Query Match 76.5%; Score 495; DB 6; Length 117;
Best Local Similarity 80.3%; Pred. No. 1.2e-38;
Matches 98; Conservative 6; Mismatches 8; Indels 10; Gaps 3;

QY 1 QVQLKESGPGLVKPSQTLITCTISGFSLSRYSVHWVROPGKGLWLGIMWGSGNTDYN 60
DB 1 QVQLKESGPGLVKPSQTLITCTISGFSLSRYSVHWVROPGKGLWLGIMWGSGNTDYN 60
QY 61 SALKSRSLISKNSKQVFLKNSLTADLTAVYYCARKEFFYYGDG-----FVYWGQGT 115
DB 61 SALKSRSLISKNSKQVFLKNSLTADLTAVYYCARKEFFYYGDG-----FVYWGQGT 115
QY 116 LV 117
DB 116 LV 117

Search completed: March 26, 2004, 05:04:04
Job time : 50.9113 secs

XX The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing *S. aureus*
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus Clf40 protein, *S. aureus* Clf33 protein, or the *S. aureus* N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is *Staphylococcus aureus* ClfA specific monoclonal
 CC antibody 12-9VLA-Hu (humanised variable light sequence) protein
 XX

Sequence 112 AA:

Query Match 100.0%; Score 583; DB 5; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4,9e-42;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMNCCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYWASTR 60
 Db 1 DIVMTQSPDLSAVSLGERVTMNCCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYWASTR 60

QY 61 ESGVPRFSGSGSGTDFTLTITSSVQAEDLAVYYCHOYLSYTFGGGTKLEIK 112
 Db 61 ESGVPRFSGSGSGTDFTLTITSSVQAEDLAVYYCHOYLSYTFGGGTKLEIK 112

RESULT 2
 AAE29266
 ID AAE29266 standard; protein; 112 AA.

AC AAE29266;
 DT 27-JAN-2003 (first entry)

XX S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.
 XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
 XX immunological; staphylococcal infection; impetigo; pneumonia; furuncles;
 XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
 XX

OS *Staphylococcus aureus*.
 XX Key Location/Qualifiers
 XX Region 24..40 /note= "CDR1"
 XX Region 56..62 /note= "CDR2"
 XX Region 95..102 /note= "CDR3"
 XX

MO200272600-A2.
 XX
 XX 19-SEP-2002.
 XX
 XX 28-JAN-2002; 2002WC-US002296.
 XX
 XX 26-JAN-2001; 2001US-0264072P.
 XX 12-MAR-2001; 2001US-0274611P.
 XX 18-JUN-2001; 2001US-0298413P.
 XX 30-JUL-2001; 2001US-0308116P.
 XX
 XX (INH1-) INHIBITEX INC.
 XX
 XX Pateti JM, Hutchins JT, Domanski P, Patel P, Hall AJ;
 XX WPI; 2002-759834/82.
 XX N-PSDB; AAD46865.
 XX
 XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
 XX treating or preventing *Staphylococcus aureus* infection e.g. wound
 XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in

PT a human or animal.
 XX
 XX Claim 11; Page 35; 80pp; English.
 XX

XX The invention relates to monoclonal antibody which binds the clumping
 CC factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA
 CC monoclonal antibody is useful for treating or preventing *S. aureus*
 CC infection in a human or animal, and for inhibiting the binding of
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
 CC S. aureus Clf40 protein, *S. aureus* Clf33 protein, or the *S. aureus* N3
 CC protein is useful for inducing an immunological response in a human or
 CC animal. These staphylococcal infections include wound infections, sepsis,
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
 CC present sequence is *Staphylococcus aureus* ClfA specific monoclonal
 CC antibody 12-9VLA-1 (variable light sequence) protein
 XX

Sequence 112 AA:

Query Match 94.9%; Score 553; DB 5; Length 112;
 Best Local Similarity 93.8%; Pred. No. 1,7e-39;
 Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMNCCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYWASTR 60
 Db 1 NIMMTQSPDLSAVSLGERVTMNCCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYWASTR 60

QY 61 ESGVPRFSGSGSGTDFTLTITSSVQAEDLAVYYCHOYLSYTFGGGTKLEIK 112
 Db 61 ESGVPRFSGSGSGTDFTLTITSSVQAEDLAVYYCHOYLSYTFGGGTKLEIK 112

RESULT 3
 AAR54933
 ID AAR54933 standard; peptide; 112 AA.

AC AAR54933;
 DT 25-MAR-2003 (revised)
 DT 19-OCT-1994 (first entry)

XX MAb 022 VK chain.
 XX
 XX Fc receptor; FcR; humanized antibody; λ ab; IgG; cancer; allergy;
 XX autoimmunity disease; heteroantibody; bifunctional antibody; immunotoxin;
 XX CDR; complementarity determining region; VH; heavy chain variable region;
 XX VK; kappa chain variable region; monoclonal phagocyte; PCR;
 XX polymerase chain reaction; primer; site-directed mutagenesis;
 XX monoclonal antibody; MAb.
 XX

OS Mus sp.
 XX
 XX MO9410332-A1.
 XX
 XX 11-MAY-1994.
 XX
 XX 04-NOV-1993; 93MO-US010384.
 XX
 XX 04-NOV-1992; 92GB-00023377.
 XX
 XX (MEDA-) MEDAREX INC.
 XX
 XX Tempest PR, Harris WJ, Carr FJ;
 XX WPI; 1994-167486/20.
 XX
 XX New humanised antibodies to Fc receptors - used for diagnosis or for
 XX treatment of e.g. cancer, allergies and infectious and auto-immune
 XX diseases.
 XX
 XX Disclosure; Page 23; 36pp; English.
 XX
 XX Humanized antibodies (λ abs) for IgG Fc receptors on human phagocytes
 XX comprise the CDR of mouse monoclonal antibody 22 (from hybridoma 022WCL-

1), VH chains from human IgE NEMW or KOL, and VK chains from Ig REI.
CC Sequences are provided for mouse 022 VH (AAR54931), humanized NEMW-based
CC VH (022 NMWH, AAR54932), humanized KOL-based VH (022 KLVH, AAR54933),
CC mouse 022 VK (AAR54933), and humanized REI-based VK (022 HVVK, AAR54932).
CC During hab production, VH and VK CDNA were PCR amplified using primers
CC given in AAR65378-87. Mutagenesis of clone M3VHPCR2 KOL VH (L71R) was
CC performed using oligos AAR65388-89. The tabs can be used in
CC heteroantibody, bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 112 AA;

Query Match 94.5%; Score 551; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2,5e-39;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMNCCKSSQSVLYSSNQKXYLAMVQKPGQSPKLLITWASTR 60
DB 1 NIMVTQSPSSLAIVAGKVTWCKSSQSVLYSSNQKXYLAMVQKPGQSPKLLITWASTR 60

QY 61 ESGVPRDFSGSGGSDFTLTITSSVQAEPLAVYYCHQYLSSTFGGSKLEIK 112
DB 61 ESGVPRDFSGSGGSDFTLTITSSVQAEPLAVYYCHQYLSSTFGGSKLEIK 112

RESULT 4
AAE29264

ID AAE29264 standard; protein; 112 AA.

AC AAE29264;

DT 27-JAN-2003 (first entry)

DE S. aureus ClfA specific monoclonal antibody 13-2VLA-1 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Region 24..40

XX Region 56..62 "CDR1"

XX Region 95..102 "CDR2"

XX Region 95..102 "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.

XX 12-MAR-2001; 2001US-0274611P.

XX 18-JUN-2001; 2001US-0298413P.

XX 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

XX Patil JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.

XX N-PSDB; AAD46863.

XX Claim 11; Page 34; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-clfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 13-2VLA-1 (variable light sequence) protein
XX

SQ Sequence 112 AA;

Query Match 93.5%; Score 545; DB 5; Length 112;
Best Local Similarity 92.0%; Pred. No. 8,1e-39;
Matches 103; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMNCCKSSQSVLYSSNQKXYLAMVQKPGQSPKLLITWASTR 60
DB 1 NIMVTQSPSSLAIVAGKVTWCKSSQSVLYSSNQKXYLAMVQKPGQSPKLLITWASTR 60

QY 61 ESGVPRDFSGSGGSDFTLTITSSVQAEPLAVYYCHQYLSSTFGGSKLEIK 112
DB 61 ESGVPRDFSGSGGSDFTLTITSSVQAEPLAVYYCHQYLSSTFGGSKLEIK 112

RESULT 5
AAE29268

ID AAE29268 standard; protein; 112 AA.

AC AAE29268;

DT 27-JAN-2003 (first entry)

DE S. aureus ClfA specific monoclonal antibody 35-220VLD-4 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Region 24..40

XX Region 56..62 "CDR1"

XX Region 95..102 "CDR2"

XX Region 95..102 "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.

XX 12-MAR-2001; 2001US-0274611P.

XX 18-JUN-2001; 2001US-0298413P.

XX 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

XX Patil JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.

XX N-PSDB; AAD46867.

XX Claim 11; Page 34; 80pp; English.

PT a human or animal.
XX
PS Claim 11, Page 37; 80pp; English.
XX
CC The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing *S. aureus*
CC infection in a human or animal, and for inhibiting the binding of
CC *Staphylococcus aureus* to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is *Staphylococcus aureus* ClfA specific monoclonal
CC antibody 35-220VLD-4 (variable light sequence) protein
XX
SQ Sequence 112 AA;
Query Match 93.3%; Score 544; DB 5; Length 112;
Best Local Similarity 92.0%; Pred. No. 9,9e-39;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQKPGQSPFLIYMASTR 60
DB 1 NIMMTQSPSSILAVSAGEKVTMCKSSQSVLYSSNOKNYLAWYQKPGQSPFLIYMASTR 60
QY 61 ESGVDPDRFGSGSGTDFLTITSSVQAEPLAVYYCHQYLSSTFGGKLEIK 112
DB 61 ESGVDPDRFGSGSGTDFLTITSSVQAEPLAVYYCHQYLSSTFGGKLEIK 112
RESULT 6
ADB97820
ID ADB97820 standard; protein; 113 AA.
XX
AC ADB97820;
XX
DT 04-DEC-2003 (first entry)
XX
DE HEV related protein #SEQ ID 14.
XX
KM Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
KM infection.
XX
OS Unidentified.
XX
PN WO2003040187-A1.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002MO-CN000797.
XX
PR 08-NOV-2001; 2001CN-00134643.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;
XX
XX WPI; 2003-441530/41.
XX
DR Hepatitis E virus monoclonal antibodies and their active fragments, for
XX use in diagnosis and developing remedies e.g. vaccines for preventing or
XX treating hepatitis E virus infection.
XX
PS Claim 2, Page 141, 165pp; Chinese.
XX
XX The invention relates to a monoclonal antibody that binds specifically to
XX hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
XX nucleotide sequences encoding the heavy-chain and/or light-chain variable
XX region of their degeneration sequences. The monoclonal antibody is
XX selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
XX CCTCC-C200116, anti-HEV monoclonal antibody 13B secreted by hybridoma
XX CCTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma

CC CCTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
CC hybridoma CCTCC-C200114. The monoclonal antibodies and their active
CC fragments are useful in diagnosis and developing remedies e.g. vaccines
CC for preventing or treating hepatitis E virus infection. From the whole
CC HEV gene obtained in patients, the HEV ORF fragment was prepared by using
CC the method of Aye et al. The polypeptide NE2 was then expressed and
CC isolated after biotechnological manipulations, which was characterized.
CC Its analogs were also produced for immunizing mice and construction of
CC hybridomas. Tests were carried out to confirm usefulness of such
CC polypeptides and monoclonal antibodies. The current sequence represents a
CC HEV related protein.
XX
SQ Sequence 113 AA;
Query Match 92.8%; Score 541; DB 7; Length 113;
Best Local Similarity 91.1%; Pred. No. 1,8e-38;
Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQKPGQSPFLIYMASTR 60
DB 1 NIMMTQSPSSILAVSAGEKVTMCKSSQSVLYSSNOKNYLAWYQKPGQSPFLIYMASTR 60
QY 61 ESGVDPDRFGSGSGTDFLTITSSVQAEPLAVYYCHQYLSSTFGGKLEIK 112
DB 61 ESGVDPDRFGSGSGTDFLTITSSVQAEPLAVYYCHQYLSSTFGGKLEIK 112
RESULT 7
AAM90226
ID AAM90226 standard; protein; 263 AA.
XX
AC AAM90226;
XX
DT 10-MAY-1999 (first entry)
XX
DE Anti-B7.2 monospecific triabody 1G10.
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
XX T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease; allergy;
XX therapy; human; triabody; antibody; 1G10.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX FT 1..24
XX FT /note= "pe1b signal peptide"
XX FT 25..144
XX FT /note= "anti B7.2 Mab VH region"
XX FT 145..257
XX FT /note= "anti B7.2 Mab VL region"
XX FT 258..263
XX FT /note= "His6 tag"
XX
XX WO9858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP003791.
XX
XX 20-JUN-1997; 97EP-00870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Lorre K, Sablon E, Buysse M, Bosman A;
XX WPI; 1999-105615/09.
XX N-PSDB; AAX01660.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection.

XX Example 7.3, Fig 34, 182pp; English.

PS This polypeptide comprises a 1G10 monospecific triabody composed of the

CC VH region of anti-B7.2 monoclonal antibody (Mab) 1G10 joined to the VL

CC region of 1G10. A triabody is a mono- or a bi- or a trispecific molecule

CC recognising simultaneously e.g. two B7.2 and one B7.1 molecules. It has

CC a rigid structure that prevents simultaneous binding to the 3 targets.

CC Each antigen-binding site is formed by pairing of one VH and one VL

CC domain from the same or from two different polypeptides. The invention

CC relates to novel molecules, including triabodies, which can cross-link

CC and/or cross-react with the costimulatory molecules B7.1 and B7.2

CC expressed on professional antigen-presenting cells, leading to the

CC inhibition of antigen-specific T cell activation. Methods are provided

CC for the production of such B7-binding molecules, and for their use in the

CC treatment or prevention of diseases of the immune system, in particular

CC graft rejection, graft versus host disease, allergy and autoimmune

CC diseases (claimed)

XX Sequence 263 AA;

XX

XX Query Match 92.6%; Score 540; DB 2; Length 263;

XX Best Local Similarity 92.0%; Pred. No. 5e-38;

XX Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSIQGERVTNCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60

DB 145 DIELTQSPSLAVSAGEEVTMTCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 204

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVOAEDLAVYYCHQYVSSYTFGGGTLEIK 112

DB 205 ESGVPDRFSGSGSGTDFTLTITSSVOAEDLAVYYCHQYVSSYTFGGGTLEIK 256

XX

XX RESULT 8

XX AAM90222 standard; protein, 268 AA.

XX ID AAM90222;

XX AC AAM90222;

XX 10-MAY-1999 (first entry)

XX DE Anti-B7.2 monospecific diabody 1G-10.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;

XX T cell activation; inhibitor; graft versus host disease;

XX transplant rejection; allograft rejection; autoimmune disease; allergy;

XX therapy; human; diabody; antibody; 1G-10.

XX Mus sp.

XX OS Synthetic.

XX OS Chimeric.

XX Key

XX Peptide 1..24

XX Location/Qualifiers

XX /note= "pe1B signal peptide"

XX 25..144

XX /note= "anti B7.2 Mab VH region"

XX 145..149

XX /note= "G4S flexible linker"

XX 150..262

XX /note= "anti B7.2 Mab VL region"

XX 263..268

XX /note= "His6 tag"

XX

XX WO9858965-A2.

XX 30-DEC-1998.

XX PD 22-JUN-1998; 98WO-EP003791.

XX PF 20-JUN-1997; 97EP-00870092.

XX PR

XX

PA (INNO-) INNOGENETICS NV.

XX

XX PI Lorre K, Sablon E, Buyse M, Bosman A;

XX WPI: 1999-105615/09.

XX DR N-PSDB; AAM01656.

XX

XX PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat

XX immune diseases including allograft rejection.

XX

XX Example 7.2, Fig 26, 182pp; English.

XX

XX This polypeptide comprises a 1G-10 monospecific diabody composed of the

XX VH region of anti-B7.2 monoclonal antibody (Mab) 1G-10 joined via a

XX short, flexible linker to the VL region of 1G-10. Mono- or bispecific

XX bivalent molecules are generated by shortening the flexible linker

XX sequence between the VH and VL of the anti-B7.1 scFv B7-24, the anti-B7.2

XX scFv 1G10 and the scFv molecule with dual specificity for B7.1 and B7.2

XX (B7.12) to 5-10 residues, and for bispecific molecules by cross-pairing

XX the VH and VL domains from the 2 scFvs with different antigen recognition

XX (B7.1/B7.2 and B7.12/B7.12). The invention relates to novel molecules,

XX including diabodies, which can cross-link and/or cross-react with the

XX costimulatory molecules B7.1 and B7.2 expressed on professional antigen-

XX presenting cells, leading to the inhibition of antigen-specific T cell

XX activation. Methods are provided for the production of such B7-binding

XX molecules, and for their use in the treatment or prevention of diseases

XX of the immune system, in particular graft rejection, graft versus host

XX disease, allergy and autoimmune diseases (claimed)

XX

XX Sequence 268 AA;

XX

XX Query Match 92.6%; Score 540; DB 2; Length 268;

XX Best Local Similarity 92.0%; Pred. No. 5.1e-38;

XX Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSIQGERVTNCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60

DB 150 DIELTQSPSLAVSAGEEVTMTCKSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 209

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVOAEDLAVYYCHQYVSSYTFGGGTLEIK 112

DB 210 ESGVPDRFSGSGSGTDFTLTITSSVOAEDLAVYYCHQYVSSYTFGGGTLEIK 261

XX

XX RESULT 9

XX AAM90228 standard; protein, 268 AA.

XX ID AAM90228;

XX AC AAM90228;

XX 10-MAY-1999 (first entry)

XX DE Anti-B7.1/anti-B7.2 bispecific triabody II.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;

XX T cell activation; inhibitor; graft versus host disease;

XX transplant rejection; allograft rejection; autoimmune disease; allergy;

XX therapy; human; triabody; antibody; B7-24; 1G10.

XX Mus sp.

XX OS Synthetic.

XX OS Chimeric.

XX Key

XX Peptide 1..39

XX Location/Qualifiers

XX /note= "g3p signal peptide"

XX 40..155

XX /note= "anti B7.1 Mab VH region"

XX 156..268

XX /note= "anti B7.2 Mab VL region"

XX

XX WO9858965-A2.

XX

PD 30-DEC-1998.
 XX 22-JUN-1998; 98MO-EP003791.
 PF 20-JUN-1997; 97EP-00870092.
 XX (INNO-) INNOGENETICS NV.
 PA Lorre K, Sablon E, Buyse M, Bosman A;
 PI WPI: 1999-105615/09.
 DR N-PSDB; AAX01662.
 XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 PT immune diseases including allograft rejection.
 PS Example 7.3; Fig 38; 182pp; English.
 CC This polypeptide comprises a bispecific triabody composed of the VH
 CC region of anti-B7.1 monoclonal antibody (Mab) B7-24 joined to the VL
 CC region of anti-B7.2 Mab 1G10. A triabody is a mono- a bi- or a
 CC trispecific molecule recognising simultaneously e.g. two B7.2 and one
 CC B7.1 molecules. It has a rigid structure that prevents simultaneous
 CC binding to the 3 targets. Each antigen-binding site is formed by pairing
 CC of one VH and one VL domain from the same or from two different
 CC polypeptides. The invention relates to novel molecules, including
 CC triabodies, which can cross-link and/or cross-react with the
 CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-
 CC presenting cells, leading to the inhibition of antigen-specific T cell
 CC activation. Methods are provided for the production of such B7-binding
 CC molecules, and for their use in the treatment or prevention of diseases
 CC of the immune system, in particular graft rejection, graft versus host
 CC disease, allergy and autoimmune diseases (claimed)
 XX Sequence 268 AA;
 SQ
 Query Match 92.6%; Score 540; DB 2; Length 268;
 Best Local Similarity 92.0%; Pred. No. 5.1e-38;
 Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIVMTGSPSLAVSLGERVTMCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLITMASTR 60
 DB 156 DIETQSPSLAVSAGEEVMTCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLITMASTR 215
 QY 61 ESGVPRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSTYFGGATKLEIK 112
 DB 216 ESGVPRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSTYFGGATKLEIK 267
 RESULT 10
 AAM90224
 ID AAM90224 standard; protein; 273 AA.
 XX AAM90224;
 AC AAM90224;
 DT 10-MAY-1999 (first entry)
 XX Anti-B7.1/anti-B7.2 bispecific diabody II.
 XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
 KM T cell activation; inhibitor; graft versus host disease;
 KM transplant rejection; allograft rejection; autoimmune disease; allergy;
 KM therapy; human; diabody; antibody; B7-24; 1G10.
 XX Mus sp.
 OS Synthetic.
 OS Chimeric.
 XX Key Location/Qualifiers
 FH Peptide 1..39 "g3p signal peptide"
 FT /note= "g3p signal peptide"
 FT Misc-difference 21
 FT /note= "encoded by TCA"

FT Region 40..155
 FT /note= "anti B7.1 Mab VH region"
 FT Peptide 156..160
 FT /note= "GAS flexible linker"
 FT Region 151..273
 FT /note= "anti B7.2 Mab VL region"
 XX WO9858965-A2.
 XX 30-DEC-1998.
 PD 22-JUN-1998; 98MO-EP003791.
 PF 20-JUN-1997; 97EP-00870092.
 XX (INNO-) INNOGENETICS NV.
 PA Lorre K, Sablon E, Buyse M, Bosman A;
 PI WPI: 1999-105615/09.
 DR N-PSDB; AAX01658.
 XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 PT immune diseases including allograft rejection.
 PS Example 7.2; Fig 30; 182pp; English.
 CC This polypeptide comprises a bispecific diabody composed of the VH region
 CC of anti-B7.1 monoclonal antibody (Mab) B7-24 joined via a short, flexible
 CC linker to the VL region of anti-B7.2 Mab 1G10. Mono- or bispecific
 CC bivalent molecules are generated by shortening the flexible linker
 CC sequence between the VH and VL of the anti-B7.1 scFv B7-24, the anti-B7.2
 CC scFv 1G10 and the scFv molecule with dual specificity for B7.1 and B7.2
 CC (B7.12) to 5-10 residues, and for bispecific molecules by cross-pairing
 CC the VH and VL domains from the 2 scFvs with different antigen recognition
 CC (B7.1/B7.2 and B7.12/B7.12). The invention relates to novel molecules,
 CC including diabodies, which can cross-link and/or cross-react with the
 CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-
 CC presenting cells, leading to the inhibition of antigen-specific T cell
 CC activation. Methods are provided for the production of such B7-binding
 CC molecules, and for their use in the treatment or prevention of diseases
 CC of the immune system, in particular graft rejection, graft versus host
 CC disease, allergy and autoimmune diseases (claimed)
 XX Sequence 273 AA;
 SQ
 Query Match 92.6%; Score 540; DB 2; Length 273;
 Best Local Similarity 92.0%; Pred. No. 5.2e-38;
 Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIVMTGSPSLAVSLGERVTMCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLITMASTR 60
 DB 161 DIETQSPSLAVSAGEEVMTCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLITMASTR 220
 QY 61 ESGVPRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSTYFGGATKLEIK 112
 DB 221 ESGVPRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSTYFGGATKLEIK 272
 RESULT 11
 AAM90218
 ID AAM90218 standard; protein; 556 AA.
 XX AAM90218;
 AC AAM90218;
 DT 10-MAY-1999 (first entry)
 XX Bispecific tetraivalent antibody B17Ab1G10-B7-24H6.
 XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
 KM T cell activation; inhibitor; graft versus host disease;
 KM transplant rejection; allograft rejection; autoimmune disease; allergy;
 KM therapy; human; bispecific tetraivalent antibody; B17Ab;

XX	BTABIG10-B7-24H6.
OS	Mus sp..
OS	Homo sapiens.
OS	Synthetic.
OS	Chimeric.
XX	
FH	Key
FT	Region
FT	Peptide
FT	Region
FT	Region
FT	Domain
FT	Domain
FT	Region
FT	Peptide
FT	Region
FT	Peptide
FT	Region
FT	Peptide
PN	W03858965-A2.
PD	30-DEC-1998.
PF	22-JUN-1998;
PR	20-JUN-1997; 97EP-00870092.
PA	(INNO-) INNOGENETICS NV.
P1	Lorrie K, Sablon E, Buysse M, Bosman A;
DR	WPI; 1999-105615/09.
DR	N-PsDB; AAX01652.
XX	
PT	New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT	immune diseases including allograft rejection.
PS	Example 7.1; Fig 18; 182pp; English.
XX	
CC	This polypeptide comprises the bispecific tetraivalent antibody BTABIG10-
CC	B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
CC	anti B7.2 scFvs (tetravalency). One single B7ab is a homodimer of 2
CC	identical molecules, each containing both an anti B7.1 and anti B7.2 scFv
CC	(bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a
CC	dimerization domain (see AA090219), which drives the homodimerisation of
CC	the molecule. DNA (see AAX01652) encoding the B7ab has been constructed
CC	to allow expression of the B7ab in transformed E. coli cells. The B7ab
CC	cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
CC	and B7.2 that are expressed on the membrane of professional antigen-
CC	presenting cells, leading to the inhibition of antigen-specific T cell
CC	activation. The invention relates to such B7-binding molecules, methods
CC	for their production, and their use for treating or preventing diseases
CC	of the immune system, in particular graft rejection, graft versus host
CC	disease, allergy and autoimmune diseases (claimed)
XX	
5Q	Sequence 556 AA:

```

Query Match      92.6%; Score 540; DB 2; Length 556;
Best Local Similarity 92.0%; Pred. No. 1-37;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0.

QY      1 DIVMTQSPDSLSAVIGERYTNCKSSQSVLYSSNQNTAMTQQKPGQSPKLLITMASR 60
      :::::::::::

```

Db	136	DIELTQSPESLAVSAGEEVTWTCCKSGSVLTKSSNKVYLAWYQCKPGQSPRLITYMASTR	136
QY	61	ESGVDPREGSGSGTDFLTITLSSVQAEADLAAYYCHQHLSSITPFGGTRLEIK	112
Db	196	ESGVDPRLFTGSGSGTDFSLTITSSVQAEADLAAYYCHQHLSSITPFGGTRLEIK	247
RESULT 12			
ID	AAW90217	standard; protein; 580 AA.	
XX	AAW90217;		
XX	10-MAY-1999	(first entry)	
DE	Bi-specific tetraivalent antibody B1TAB7-24-1G10H6.		
XX	B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;		
KW	T cell activation; inhibitor; graft versus host disease;		
KW	transplant rejection; allograft rejection; autoimmune disease; allergy;		
KM	therapy; human; bi-specific tetraivalent antibody; B1Tab;		
KX	B1TAB7-24-1G10H6.		
XX			
OS	Mus sp.		
OS	Homo sapiens.		
OS	Synthetic.		
XX	Chimeric.		
XX			
XX	Key	Location/Qualifiers	
FT	Peptide	1..24	
FT		/note="peB signal peptide"	
FT	Region	25..138	
FT		/note="VH region anti B7.1 Mab"	
FT	Peptide	139..153	
FT		/note="(G4S3) flexible linker"	
FT	Region	154..262	
FT		/note="VL region anti B7.1 Mab"	
FT	Misc-difference	261	
FT		/note="encoded by CTG"	
FT	Region	263..273	
FT		/note="human IgG3 hinge region"	
FT	Domain	274..308	
FT		/note="helix-turn-helix dimerisation domain"	
FT	Domain	309..319	
FT		/note="human IgG3 hinge domain"	
FT	Region	320..446	
FT		/note="VH region anti B7.2 Mab"	
FT	Misc-difference	322..327	
FT		/note="codons for these amino acids are not present in the DNA sequence for B1TAB7-24-1G1-H6 provided in the specification"	
FT	Peptide	447..461	
FT		/note="(G4S3)flexible linker"	
FT	Region	462..574	
FT		/note="VL region anti B7.2 Mab"	
FT	Peptide	575..580	
FT		/note="His6 tag"	
XX			
PN	W09858965-A2.		
XX			
PD	30-DEC-1998.		
XX			
PF	22-JUN-1998;	98MO-EP003791.	
XX			
PR	20-JUN-1997;	97EP-00870092.	
XX			
PA	(INNO-) INNOGENETICS NV.		
XX			
PI	Lorrie K, Sablon E, Buyse M, Bosman A;		
XX			
DR	WPI; 1999-105615/09.		
XX	DR N-PsDB; AAX01651.		

PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 XX immune diseases including allograft rejection.
 PS Example 7.1, Fig 16, 182pp; English.

XX This polypeptide comprises the bispecific tetravalent antibody B1TabB7.24
 CC -1G10H6. The molecule consists of 4 scfvs, 1.e. 2 anti B7.1 scfvs and 2
 CC anti B7.2 scfvs (tetra-avalency). One single B1Tab is a homodimer of 2
 CC identical molecules, each containing both an anti B7.1 and anti B7.2 scfv
 CC (bispecificity). An anti-B7.1 and anti-B7.2 scfv are linked using a
 CC dimerisation domain (see AAW90219), which drives the homodimerisation of
 CC the molecule. DNA (see AAW901651) encoding the B1Tab has been constructed
 CC to allow expression of the B1Tab in transformed E. coli cells. The B1Tab
 CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
 CC and B7.2 that are expressed on the membrane of professional antigen-
 CC presenting cells, leading to the inhibition of antigen-specific T cell
 CC activation. The invention relates to such B7-binding molecules, methods
 CC for their production, and their use for treating or preventing diseases
 CC of the immune system, in particular graft rejection, graft versus host
 CC disease, allergy and autoimmune diseases (claimed)

XX Sequence 580 AA;

Query Match 92.6%; Score 540; DB 2; Length 580;
 Best Local Similarity 92.0%; Pred. No. 1,1e-37;
 Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIWVTGSPDLSAVSLGRRVTMCKSSQSVLYSSNQKYLAMVQKPGQSPKLLIYNASTR 60
 DB 462 DIETLSPSSILAVSAGEEVTMTCKSSQSVLYSSNQKYLAMVQKPGQSPKLLIYNASTR 521

QY 61 ESGVPRDFSSGSGGTFDLTITSSVOAEDLAVYCHQYLSSYTFGGTKLEIK 112
 DB 522 ESGVPRDFSSGSGGTFDLTITSSVOAEDLAVYCHQYLSSYTFGGTKLEIK 573

RESULT 13
 ABG31024
 ID ABG31024 standard; protein; 272 AA.

AC ABG31024;

XX 05-NOV-2002 (first entry)

XX Synthetic mouse fusion protein.

XX Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse;
 KW neuroprotective; gene therapy; single chain antibody; variable fragment;
 KW Bcrv; binding domain-immunoglobulin fusion protein; B-cell disorder;
 KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
 KW Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;
 KW multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;
 KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
 KW ulcerative colitis; inflammatory bowel disease; immunological effector;
 KW cell mediated cytotoxicity; complement dependent cytotoxicity;
 KW complement fixation; mouse.

XX Mus musculus.
 OS Synthetic.

XX WO200256910-A1.

XX 25-JUL-2002.

XX 17-JAN-2002; 2002WO-US001487.

XX 17-JAN-2001; 2001US-00765208.

XX (GENE-) GENE-CRAFT INC.

XX Ledbetter JA, Hayden-Ledbetter M;

XX WPI; 2002-599691/64.

DR N-PSDB; ABK89856.
 XX New human binding domain-immunoglobulin fusion protein useful for
 PT treating a subject having or suspected of having a B-cell disorder or
 PT malignant condition e.g. rheumatoid arthritis.
 PS Disclosure; Page 119; 136pp; English.

XX The invention describes a binding domain-immunoglobulin fusion protein
 CC that is capable of at least one immunological activity, comprising a
 CC binding domain polypeptide fused to an immunoglobulin hinge region
 CC polypeptide capable of specifically binding to an antigen, or an
 CC immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused
 CC to the hinge region polypeptide or to the CH2 constant region
 CC polypeptide. The fusion protein is useful for treating a subject having
 CC or suspected of having a B-cell disorder or malignant condition e.g.
 CC rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's
 CC thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
 CC erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura,
 CC psoriasis, scleroderma, cancer and inflammatory bowel disease such as
 CC Chron's disease and ulcerative colitis. The fusion protein retains the
 CC ability to participate in well known immunological effector activities
 CC including antibody dependent cell mediated cytotoxicity and/or complement
 CC fixation in complement dependent cytotoxicity, despite having structures
 CC that would not be expected to be capable of promoting the effector
 CC activities. It can be produced in substantial quantities that are
 CC typically greater than those routinely attained with single-chain
 CC antibody constructs. This is the amino acid sequence of a synthetic mouse
 CC immunoglobulin fusion protein

XX Sequence 272 AA;

Query Match 91.4%; Score 533; DB 5; Length 272;
 Best Local Similarity 89.3%; Pred. No. 2e-37;
 Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIWVTGSPDLSAVSLGRRVTMCKSSQSVLYSSNQKYLAMVQKPGQSPKLLIYNASTR 60
 DB 21 NIMVTGSPSSILAVSAGEEVTMTCKSSQSVLYSSNQKYLAMVQKPGQSPKLLIYNASTR 80

QY 61 ESGVPRDFSSGSGGTFDLTITSSVOAEDLAVYCHQYLSSYTFGGTKLEIK 112
 DB 81 ESGVPRDFSSGSGGTFDLTITSSVOAEDLAVYCHQYLSSYTFGGTKLEIK 132

RESULT 14

ADD25453
 ID ADD25453 standard; protein; 272 AA.

AC ADD25453;

XX 15-JAN-2004 (first entry)

XX Binding domain-immunoglobulin fusion protein-associated protein #4.

XX Binding domain: immunoglobulin; fusion protein; cytostatic;
 KW antitumor; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; 19g1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

XX US2003118592-A1.

XX 26-JUN-2003.

XX 25-JUL-2002; 2002US-00207655.

XX 17-JAN-2001; 2001US-0367358P.

PR 17-JUN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 PA (GENE-) GENE-CRAFT INC.
 PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 XX WPI, 2003-801317/75.
 DR
 XX
 PT New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 14; 157pp; English.

CC The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues, where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic form of directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID
 CC number therefore none of the sequences can be explicitly identified.
 XX

SO Sequence 272 AA;

Query Match 91.4%; Score 533; DB 7; Length 272;
 Best Local Similarity 89.3%; Pred. No. 2e-37;
 Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVVTGSPDLSAVLGERVTMNCSSQSVLYSSNOKRYLAWYQKPGQSPKLLITVMASTR 60
 Db 21 NIKMTSPSSSLAVSAGEKVTMNCSSQSVLYSSNOKRYLAWYQKPGQSPKLLITVMASTR 80
 QY 61 ESGVDPDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTLEIK 112
 Db 81 ESGVDPDRFSGSGSGTDFTLTISVHTEDLAVYYCHQFLSSMTFGGTLEIK 132

RESULT 15
 AAR92215

ID AAR92215 standard; protein; 113 AA.
 XX
 AC AAR92215;
 XX
 DT 28-MAY-1996 (first entry)
 XX
 DE LL2 MAb VR region.
 XX
 XX Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;
 KW leukaemia; therapy; diagnosis; complementarity determining region; CDR;
 KW antibody engineering.
 XX
 OS Mus musculus.

XX Location/Qualifiers
 FH 24..40
 FT Region
 FT /label= CDR1
 FT /note= "claim 6, page 44"
 FT 56..62
 FT Region
 FT /label= CDR2
 FT /note= "claim 7, page 44"
 FT 95..103
 FT Region
 FT /label= CDR3
 FT /note= "claim 8, page 44"

PN MO9604925-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 11-AUG-1995; 95WO-05009641.
 XX
 PR 12-AUG-1994; 94US-00289576.
 XX

PA (IMMU-) IMMUNOMEDICS INC.

PI Leung S, Hansen H;
 XX
 XX WPI; 1996-139454/14.
 DR
 DR N-PSDB; AAT15802.

PT Chimeric and humanised LL2 antibodies - used to produce conjugates for
 PT the therapy and diagnosis of B-cell lymphoma(s) and leukaemia(s).

PS Claim 5; Page 35-36; 70pp; English.

CC The complementarity determining regions (CDRs) of mouse monoclonal
 CC antibody (MAb) LL2 VR (AAR92215) and VH (AAR92216) regions were
 CC recombinantly linked to the framework sequences of human VK and VH
 CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 CC (AAR92218). These were subsequently linked, respectively, to human kappa
 CC and IgG1 constant regions. A humanised MAb was obtained that retained the B-
 CC lymphoma and leukaemia cell targeting and internalisation characteristics
 CC of the parental LL2 MAb, and which exhibited a lowered HAMA reaction. It
 CC can be linked to e.g. a cytostatic agent for therapeutic appln
 XX

SO Sequence 113 AA;

Query Match 90.4%; Score 527; DB 2; Length 113;
 Best Local Similarity 88.4%; Pred. No. 2.8e-37;
 Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVVTGSPDLSAVLGERVTMNCSSQSVLYSSNOKRYLAWYQKPGQSPKLLITVMASTR 60
 Db 1 DIQLTGSPSSSLAVSAGENVTMNCSSQSVLYSSNOKRYLAWYQKPGQSPKLLITVMASTR 60
 QY 61 ESGVDPDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTLEIK 112
 Db 61 ESGVDPDRFSGSGSGTDFTLTISVQVEDLAVYYCHQYLSSMTFGGTLEIK 112

Search completed: March 26, 2004, 05:03:59
 Job time : 46.4965 secs

RESULT 2
US-08-690-102A-2
Sequence 2, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-2

Query Match 90.4%; Score 527; DB 1; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVWTQSPDSLAVSLGERVTMNCSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIQLTQSPDSLAVSAGENVMTSCSSQSVLYSANHKNYLAWYQKPGQSPKLLIYMASTR 60

QY 61 ESGVPRDRSGSGSGTDFLTITISVQAEFLAVYYCHQYLSYTFGGGTLEIK 112
DB 61 ESGVPRDRSGSGSGTDFLTITISVQAEFLAVYYCHQYLSYTFGGGTLEIK 112

RESULT 3
US-09-127-902-2
Sequence 2, Application US/09127902
Patent No. 6187287
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-JUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-902-2

Query Match 90.4%; Score 527; DB 3; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVWTQSPDSLAVSLGERVTMNCSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIQLTQSPDSLAVSAGENVMTSCSSQSVLYSANHKNYLAWYQKPGQSPKLLIYMASTR 60

QY 61 ESGVPRDRSGSGSGTDFLTITISVQAEFLAVYYCHQYLSYTFGGGTLEIK 112
DB 61 ESGVPRDRSGSGSGTDFLTITISVQAEFLAVYYCHQYLSYTFGGGTLEIK 112

RESULT 4
US-09-155-107-2
Sequence 2, Application US/09155107
Patent No. 6254868
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: OU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/0879
CURRENT APPLICATION NUMBER: US/09/155,107
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: WO PCT/US97/04196
EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: US 60/013,709
EARLIER FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murine
US-09-155-107-2

Query Match 90.4%; Score 527; DB 3; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVWTQSPDSLAVSLGERVTMNCSSQSVLYSSNOKNYLAWYQKPGQSPKLLIYMASTR 60

Db 1 D1QLTQSPSLAVSAGENVMTSCSSQSVLYSNHKNVLAHYQKQKQSPKLLIYMASTR 60

Qy 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112
Db 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112

RESULT 5

PCT-US95-09641-2
Sequence 2, Application PC/TUS9509641
GENERAL INFORMATION:

TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09641
FILING DATE: 11-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US95-09641-2

Query Match 90.4%; Score 527; DB 5; Length 113;
Best Local Similarity 88.4%; Pred. No. 2, 5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 D1VMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNVLAHYQKQKQSPKLLIYMASTR 60
Db 1 D1QLTQSPSLAVSAGENVMTSCSSQSVLYSNHKNVLAHYQKQKQSPKLLIYMASTR 60

Qy 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112
Db 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112

Qy 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112
Db 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112

RESULT 6

PCT-US93-08435-6
Sequence 6, Application PC/TUS9308435
GENERAL INFORMATION:

APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of

APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of

TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road

CITY: Spring House
STATE: PA
COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US93-08435-6

Query Match 90.1%; Score 525.5; DB 5; Length 113;
Best Local Similarity 90.3%; Pred. No. 3, 5e-42;
Matches 102; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 D1VMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNVLAHYQKQKQSPKLLIYMASTR 60
Db 1 D1VMTQSPDSLAVSLGERATINCKSSQSVLYSSNKNVLAHYQKQKQSPKLLIYMASTR 60

Qy 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112
Db 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112

Qy 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112
Db 61 ESVGPRFSSGSGGTDTLTITSSVQADLAHYCHQYLSYTTGGGTKEIK 112

RESULT 7

US-07-942-245-30
Sequence 30, Application US/07942245
Patent No. 5639641

GENERAL INFORMATION:

APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M. J.

APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.

TITLE OF INVENTION: BRAYDON C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington
STATE: D.C.

COUNTRY: United States
ZIP: 20037-3202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX

SOFTWARE: In house
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992

CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860

TELEX: 6491103
INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-942-245-30

Query Match 89.4%; Score 521; DB 1; Length 112;

Best Local Similarity 89.3%; Pred. No. 9e-42; Mismatches 100; Conservative 5; Indels 7; Gaps 0;

QY 1 DIVWTQSPDLSAVSGERVNCKSSQSVLYSSNOKRYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIVWTQSPDLSAVSGERVNCKSSQSVLYSSNOKRYLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVDPDRFSGSGGSDTFTLTITSSVQAEADLAVYYCHQYLSSYTFGGTKLEIK 112
DB 61 ESGVDPDRFSGSGGSDTFTLTITSSVQAEADLAVYYCHQYLSSYTFGGTKLEIK 112

RESULT 8
US-07-916-098A-15Sequence 15, Application US/07916098A
Patent No. 5871732

GENERAL INFORMATION:

APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.

APPLICANT: ROSA, JOSEPH J.

TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVECITY: CHICAGO
STATE: ILLINOIS

COUNTRY: U.S.A.

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/916,098A

FILING DATE: July 24, 1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/08843

FILING DATE: No. 5871732, September 27, 1991

CLASSIFICATION: 424

APPLICATION NUMBER: 07/618,542

FILING DATE: No. 5871732, September 27, 1990

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: JOHN J. MC DONNELL

REGISTRATION NUMBER: 26,949

REFERENCE/DOCKET NUMBER: 92,310-G

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 715-1000

TELEFAX: (312) 715-1234

TELEX: 910/221-5317

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-916-098A-15

Query Match 89.4%; Score 521; DB 2; Length 112;

Best Local Similarity 89.3%; Pred. No. 9e-42; Mismatches 100; Conservative 6; Indels 0; Gaps 0;

QY 1 DIVWTQSPDLSAVSGERVNCKSSQSVLYSSNOKRYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIVWTQSPDLSAVSGERVNCKSSQSVLYSSNOKRYLAWYQKPGQSPKLLIYMASTR 60

DB 1 DIVWTQSPDLSAVSGERVNCKSSQSVLYSSNOKRYLAWYQKPGQSPKLLIYMASTR 60

QY 61 ESGVDPDRFSGSGGSDTFTLTITSSVQAEADLAVYYCHQYLSSYTFGGTKLEIK 112

DB 61 ESGVDPDRFSGSGGSDTFTLTITSSVQAEADLAVYYCHQYLSSYTFGGTKLEIK 112

RESULT 9
US-09-274-163E-16Sequence 16, Application US/09274163E
Patent No. 6485943

GENERAL INFORMATION:

APPLICANT: STEVENS, Fred J.

APPLICANT: WILKINS STEVENS, Patricia

APPLICANT: RAPPEN, Rosemarie

APPLICANT: SCHIFFER, Marianne

TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION

FILE REFERENCE: 051583/0224

CURRENT APPLICATION NUMBER: US/09/274,163E

CURRENT FILING DATE: 1999-03-22

PRIOR APPLICATION NUMBER: US 08/373,380

PRIOR FILING DATE: 1995-01-17

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patent in version 3.1

SEQ ID NO 16

LENGTH: 113

TYPE: PRF

ORGANISM: Escherichia coli

US-09-274-163E-16

Query Match 89.3%; Score 520.5; DB 4; Length 113;

Best Local Similarity 89.4%; Pred. No. 1e-41; Mismatches 101; Conservative 5; Indels 6; Gaps 1;

QY 1 DIVWTQSPDLSAVSGERVNCKSSQSVLYSSNOKRYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIVWTQSPDLSAVSGERVNCKSSQSVLYSSNOKRYLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVDPDRFSGSGGSDTFTLTITSSVQAEADLAVYYCHQYLSSYTFGGTKLEIK 112
DB 61 ESGVDPDRFSGSGGSDTFTLTITSSVQAEADLAVYYCHQYLSSYTFGGTKLEIK 112

RESULT 10
PCT-US93-08435-8Sequence 8, Application PC/TUS9308435
GENERAL INFORMATION:

APPLICANT: SmithKline Beecham, Corporation

APPLICANT: U. S. Government, Secretary of

APPLICANT: the Navy

APPLICANT: U. S. Government, Secretary of

APPLICANT: the Army

TITLE OF INVENTION: Novel Antibodies for Confering Passive

TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Box 457, 321 Norristown Road

CITY: Spring House

STATE: PA

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08435

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,654

FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-8

Query Match 89.3%; Score 520.5; DB 5; Length 113;
Best Local Similarity 89.4%; Pred. No. 1e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNYLAAYVYQKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNYLAAYVYQKPGQSPKLLIYMASTR 60
QY 61 ESGVPRFSGSGSGTDFTLTISSVQAEDLAAYVYCHQYLS-YTFGGGTGLEIK 112
DB 61 ESGVPRFSGSGSGTDFTLTISSVQAEDLAAYVYCHQYLS-YTFGGGTGLEIK 112

RESULT 11

US-08-828-741B-11

Sequence 11, Application US/08828741B

Patent No. 6043069

GENERAL INFORMATION:

APPLICANT: Koentgen, Frank

APPLICANT: Suess, Gabriele M.

APPLICANT: Tarlinton, David M.

APPLICANT: Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF

NUMBER OF INVENTION: PRODUCING SAME

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,741B

FILING DATE: 26-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10591

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 155 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-828-741B-11

Query Match 89.3%; Score 520.5; DB 3; Length 155;
Best Local Similarity 89.4%; Pred. No. 1.4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNYLAAYVYQKPGQSPKLLIYMASTR 60
DB 30 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNYLAAYVYQKPGQSPKLLIYMASTR 89
QY 61 ESGVPRFSGSGSGTDFTLTISSVQAEDLAAYVYCHQYLS-YTFGGGTGLEIK 112
DB 90 ESGVPRFSGSGSGTDFTLTISSVQAEDLAAYVYCHQYLS-YTFGGGTGLEIK 142

RESULT 12

US-09-160-567-11

Sequence 11, Application US/09160567

Patent No. 6326179

GENERAL INFORMATION:

APPLICANT: Koentgen, Frank

APPLICANT: Suess, Gabriele M.

APPLICANT: Tarlinton, David M.

APPLICANT: Treutlein, Herbert R.

TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF

NUMBER OF INVENTION: PRODUCING SAME

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/160,567

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,741

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10591

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 155 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-160-567-11

Query Match 89.3%; Score 520.5; DB 4; Length 155;
Best Local Similarity 89.4%; Pred. No. 1.4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNYLAAYVYQKPGQSPKLLIYMASTR 60
DB 30 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNKNYLAAYVYQKPGQSPKLLIYMASTR 89
QY 61 ESGVPRFSGSGSGTDFTLTISSVQAEDLAAYVYCHQYLS-YTFGGGTGLEIK 112
DB 90 ESGVPRFSGSGSGTDFTLTISSVQAEDLAAYVYCHQYLS-YTFGGGTGLEIK 142

RESULT 13
US-09-710-299-11
Sequence 11, Application US/09710299
Patent No. 6521741
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
Suess, Gabriele M.
Tarlington, David M.
Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/710,299
FILING DATE: 09-No. 6521741-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-710-299-11
Query Match 89.3%; Score 520.5; DB 4; Length 155;
Best Local Similarity 89.4%; Pred. No. 1,4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
QY 1 DIVWTQSPDSLAVSLGERVTMNCSSQSVLYSSNOKRYLAWYQOKPQSPKLLIYMASTR 60
DB 30 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNRYLAWYQOKPQSPKLLIYMASTR 89
QY 61 ESGVPDRFSGSGGTDFLTLLISSVQAEADLAVYYCHQYLLS-YTFGGGTGLEIK 112
DB 90 ESGVPDRFSGSGGTDFLTLLISSVQAEADLAVYYCHQYLLS-YTFGGGTGLEIK 142
RESULT 14
US-09-509-031-11
Sequence 11, Application US/09509031
Patent No. 659080
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
Suess, Gabriele M.
Tarlington, David M.
Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/09/509,031

CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 155
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kappa
US-09-509-031-11
Query Match 89.3%; Score 520.5; DB 4; Length 155;
Best Local Similarity 89.4%; Pred. No. 1,4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
QY 1 DIVWTQSPDSLAVSLGERVTMNCSSQSVLYSSNOKRYLAWYQOKPQSPKLLIYMASTR 60
DB 30 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNRYLAWYQOKPQSPKLLIYMASTR 89
QY 61 ESGVPDRFSGSGGTDFLTLLISSVQAEADLAVYYCHQYLLS-YTFGGGTGLEIK 112
DB 90 ESGVPDRFSGSGGTDFLTLLISSVQAEADLAVYYCHQYLLS-YTFGGGTGLEIK 142
RESULT 15
US-08-828-741B-6
Sequence 6, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
Suess, Gabriele M.
Tarlington, David M.
Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-741B-6
Query Match 89.3%; Score 520.5; DB 3; Length 342;
Best Local Similarity 89.4%; Pred. No. 3,4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIWTOGSPDIAVSLGERVTMNCSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 30 DIWTOGSPDIAVSLGERATINCKSSQSVLYSSNSXNYLAWYQOKPGQSPKLLIYMASTR 89
QY 61 ESGVDPDRFSGSGGTDFTLTISGVAEDLAVYCHQYLSS-YTFGGGTLEIK 112
Db 90 ESGVDPDRFSGSGGTDFTLTISLQAEDVAVYCCQYISTPYSTFGGTLEIK 142

Search completed: March 26, 2004, 05:11:18
Job time : 41.7163 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 05:07:57 ; Search time 353.277 Seconds

(without alignments)
82.955 Million cell updates/sec

Title: US-10-056-052a-18

Perfect score: 583
Sequence: 1 DIVMTQSPDLSLVISGERVT.....YCHQYLSSYTFGGTKLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/1/pubpaa/PCTUS_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	583	100.0	112	14	US-10-056-052-18
2	553	94.9	112	14	US-10-056-052-10
3	551	94.5	112	14	US-10-229-335-28
4	545	93.5	112	14	US-10-056-052-6
5	544	93.3	112	14	US-10-056-052-14
6	533	91.4	272	14	US-10-207-655-14
7	533	91.4	272	14	US-10-053-530-14
8	527	90.4	113	9	US-09-741-843-2
9	527	90.4	113	10	US-09-894-839-2
10	527	90.4	113	10	US-09-988-013A-2
11	520.5	89.3	113	15	US-10-446-689-2
12	520.5	89.3	113	9	US-09-274-163B-16
13	520.5	89.3	155	14	US-10-345-618-11
14	520.5	89.3	342	14	US-10-345-618-6
15	520.5	89.3	495	14	US-10-345-618-4

16	516.5	88.6	113	14	US-10-255-478-73	Sequence 73, Appl
17	516.5	88.6	114	9	US-09-274-163B-2	Sequence 2, Appl
18	516.5	88.6	114	9	US-09-274-163B-6	Sequence 6, Appl
19	516	88.5	130	13	US-10-146-305-7	Sequence 7, Appl
20	515.5	88.4	114	9	US-09-274-163B-4	Sequence 4, Appl
21	513.5	88.1	113	9	US-09-956-206A-80	Sequence 80, Appl
22	512.5	87.9	134	14	US-10-255-478-58	Sequence 58, Appl
23	512.5	87.9	240	9	US-09-799-514-8	Sequence 8, Appl
24	512.5	87.9	274	14	US-10-255-478-66	Sequence 66, Appl
25	510.5	87.6	113	10	US-09-995-529-6	Sequence 6, Appl
26	510.5	87.6	119	14	US-10-010-722-13	Sequence 13, Appl
27	510	87.5	141	14	US-10-390-986-18	Sequence 16, Appl
28	507.5	87.0	114	9	US-09-810-502-38	Sequence 38, Appl
29	507.5	87.0	264	15	US-10-264-049-4274	Sequence 4274, Ap
30	506.5	86.9	126	14	US-10-255-478-64	Sequence 64, Appl
31	506.5	86.9	284	14	US-10-255-478-70	Sequence 70, Appl
32	505.5	86.7	132	14	US-10-010-729-51	Sequence 51, Appl
33	503.5	86.4	113	14	US-10-121-464-6	Sequence 6, Appl
34	503.5	86.4	113	14	US-10-159-006-6	Sequence 34, Appl
35	503.5	86.4	113	14	US-10-159-006-34	Sequence 11, Appl
36	503.5	86.4	114	14	US-10-125-687-11	Sequence 1, Appl
37	502.5	86.2	135	14	US-10-171-452A-1	Sequence 1, Appl
38	502.5	86.2	135	15	US-10-353-708-1	Sequence 6, Appl
39	500	85.8	113	9	US-09-741-843-6	Sequence 6, Appl
40	500	85.8	113	10	US-09-894-839-6	Sequence 6, Appl
41	500	85.8	113	10	US-09-988-013A-6	Sequence 6, Appl
42	500	85.8	113	15	US-10-446-689-6	Sequence 6, Appl
43	499.5	85.7	113	14	US-10-121-464-2	Sequence 2, Appl
44	499.5	85.7	113	14	US-10-159-006-2	Sequence 2, Appl
45	499.5	85.7	113	14	US-10-159-006-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-10-056-052-18
Sequence 18, Application US/10056052
Publication No. US2003009656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE C1FA PROTEIN
FILE REFERENCE: PCT069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/299,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-18

Query Match 100.0%; Score 583; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. NO. 4.3e+48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMTQSPDLSLVISGERVTNNCKSSQSVLYSSNQKYLAWYQQKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDLSLVISGERVTNNCKSSQSVLYSSNQKYLAWYQQKPGQSPKLLIYMASTR 60

QY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112
DB 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112

RESULT 2
US-10-056-052-10

Sequence 10, Application US/10056052
Publication No. US2003009656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P070690504/BAS
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 10
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match 94.5%; Score 553; DB 14; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.1e-45;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVWTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKNTLAWYQKPGQSPFLTIYMASTR 60
1 NIMWTQSPDSLAVSAGEKVTWNCSSQSVLYSSNQKNTLAWYQKPGQSPFLTIYMASTR 60
DB 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112
61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112

RESULT 3
US-10-229-335-28

Sequence 28, Application US/10229335
Publication No. US2003014483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
IMMUNOGLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P O. Box 953, 1545 Route 22 East
CITY: Amundale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match 94.5%; Score 551; DB 14; Length 112;
Best Local Similarity 93.8%; Pred. No. 4.8e-45;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVWTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKNTLAWYQKPGQSPFLTIYMASTR 60
1 NIMWTQSPDSLAVSAGEKVTWNCSSQSVLYSSNQKNTLAWYQKPGQSPFLTIYMASTR 60
DB 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112
61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112

RESULT 4
US-10-056-052-6

Sequence 6, Application US/10056052
Publication No. US2003009656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P070690504/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 6
LENGTH: 112
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match 93.5%; Score 545; DB 14; Length 112;
Best Local Similarity 92.0%; Pred. No. 1.8e-44;
Matches 103; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVWTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKNTLAWYQKPGQSPFLTIYMASTR 60
1 NIMWTQSPDSLAVSAGEKVTWNCSSQSVLYSSNQKNTLAWYQKPGQSPFLTIYMASTR 60
DB 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112
61 ESGVDPDRFSGSGGTDFLTITSSVQAEADLAVYYCHQYLSSYTFGGGTLEIK 112

RESULT 5

US-10-056-052-14
; Sequence 14, Application US/10056052
; Publication No. US20030099656a1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-14

Query Match 93.3%; Score 544; DB 14; Length 112;
Best Local Similarity 92.0%; Pred. No. 2.2e-44;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSIAVSIGERYTNKCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
DB 1 NIMMTQSPSLAVSAGEKYTNCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTLEIK 112
DB 61 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTLEIK 112

RESULT 6

US-10-207-655-14
; Sequence 14, Application US/10207655
; Publication No. US20030118592a1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-207-655-14

Query Match 91.4%; Score 533; DB 14; Length 272;
Best Local Similarity 89.3%; Pred. No. 6.6e-43;
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSIAVSIGERYTNKCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
DB 1 NIMMTQSPSLAVSAGEKYTNCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60

DB 21 NIMMTQSPSLAVSAGEKYTNCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 80

QY 61 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTLEIK 112
DB 81 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTLEIK 132

RESULT 7

US-10-053-530-14
; Sequence 14, Application US/10053530
; Publication No. US20030133939a1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401
; CURRENT APPLICATION NUMBER: US/10/053,530
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(272)
; OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-053-530-14

Query Match 91.4%; Score 533; DB 14; Length 272;
Best Local Similarity 89.3%; Pred. No. 6.6e-43;
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSIAVSIGERYTNKCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
DB 21 NIMMTQSPSLAVSAGEKYTNCKSSQSVLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 80
QY 61 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTLEIK 112
DB 81 ESGVPRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSYTFGGGTLEIK 132

RESULT 8

US-09-741-843-2
; Sequence 2, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-741-843-2

Query Match 90.4%; Score 527; DB 9; Length 113;
Best Local Similarity 88.4%; Pred. No. 9.5e-43;

Mon Mar 29 10:05:45 2004

us-10-056-052a-18.rapb

Page 4

Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVTQSPDLSLAVSLGERVTMCKSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIQTQSPSSSLAVSAGENVMTSCSKSQSVLYSANHKXYLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112
DB 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112

RESULT 9
US-09-894-839-2
Sequence 2, Application US/09894839
Publication No. US20030035800A1

GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
APPLICANT: QU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
FILE REFERENCE: 018733/1049
CURRENT APPLICATION NUMBER: US/09/894,839
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/155,107
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/013,709
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-894-839-2

Query Match 90.4%; Score 527; DB 10; Length 113;
Best Local Similarity 88.4%; Pred. No. 9.5e-43;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVTQSPDLSLAVSLGERVTMCKSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIQTQSPSSSLAVSAGENVMTSCSKSQSVLYSANHKXYLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112
DB 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112

RESULT 10
US-09-988-013A-2
Sequence 2, Application US/09888013A
Publication No. US20030103579A1
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
FILE REFERENCE: 18733/1082
CURRENT APPLICATION NUMBER: US/09/988,013A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 09/741,843
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-06
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT

ORGANISM: Murinae gen. sp.
US-09-988-013A-2

Query Match 90.4%; Score 527; DB 10; Length 113;
Best Local Similarity 88.4%; Pred. No. 9.5e-43;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVTQSPDLSLAVSLGERVTMCKSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIQTQSPSSSLAVSAGENVMTSCSKSQSVLYSANHKXYLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112
DB 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112

RESULT 11
US-10-446-689-2
Sequence 2, Application US/10446689
Publication No. US20040013607A1

GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL LYME
FILE REFERENCE: 18733/1234
CURRENT APPLICATION NUMBER: US/10/446,689
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: US 09/741,843
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/127,902
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/690,102
PRIOR FILING DATE: 1996-07-31
PRIOR APPLICATION NUMBER: US 08/289,576
PRIOR FILING DATE: 1994-08-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 113
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-10-446-689-2

Query Match 90.4%; Score 527; DB 15; Length 113;
Best Local Similarity 88.4%; Pred. No. 9.5e-43;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVTQSPDLSLAVSLGERVTMCKSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIQTQSPSSSLAVSAGENVMTSCSKSQSVLYSANHKXYLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112
DB 61 ESGVPRFSGSGGTDTFTLTSSVQAEADLAVYCHQYLSSTFGGKLEIK 112

RESULT 12
US-09-274-163E-16
Sequence 16, Application US/09274163E
Patent No. US20020137897A1
GENERAL INFORMATION:
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFFEN, Rosemarie
APPLICANT: SCHIFFER, Marianne
TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
FILE REFERENCE: 051583/0224
CURRENT APPLICATION NUMBER: US/09/274,163E
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 08/373,380
PRIOR FILING DATE: 1995-01-17
NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 113
TYPE: PRT
ORGANISM: Escherichia coli*
US-09-274-163E-16

Query Match 89.3%; Score 520.5; DB 9; Length 113;
Best Local Similarity 89.4%; Pred. No. 3.9e-42;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVWTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 1 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNSKXYLAWYQKPGQSPKLLIYMASTR 60
QY 61 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 112
DB 61 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 113

RESULT 13
US-10-345-618-11
Sequence 11, Application US/10345618
Publication No. US20030148484A1

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tatinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBIODES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 155
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kappa
OTHER INFORMATION: protein sequence
US-10-345-618-11

Query Match 89.3%; Score 520.5; DB 14; Length 155;
Best Local Similarity 89.4%; Pred. No. 5.5e-42;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVWTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 30 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNSKXYLAWYQKPGQSPKLLIYMASTR 89
QY 61 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 112
DB 90 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 142

RESULT 14

US-10-345-618-6
Sequence 6, Application US/10345618
Publication No. US20030148484A1

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tatinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBIODES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031

PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 342
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TML protein
OTHER INFORMATION: sequence
US-10-345-618-6

Query Match 89.3%; Score 520.5; DB 14; Length 342;
Best Local Similarity 89.4%; Pred. No. 1.3e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVWTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 30 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNSKXYLAWYQKPGQSPKLLIYMASTR 89
QY 61 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 112
DB 90 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 142

RESULT 15

US-10-345-618-4
Sequence 4, Application US/10345618
Publication No. US20030148484A1

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tatinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBIODES AND A METHOD OF PRODUCING SAME
FILE REFERENCE: 13474
CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 495
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CATAB-TRV
OTHER INFORMATION: protein sequence
US-10-345-618-4

Query Match 89.3%; Score 520.5; DB 14; Length 495;
Best Local Similarity 89.4%; Pred. No. 2e-41; 6; Indels 1; Gaps 1;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVWTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKXYLAWYQKPGQSPKLLIYMASTR 60
DB 30 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNSKXYLAWYQKPGQSPKLLIYMASTR 89
QY 61 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 112
DB 90 ESGVPRFRSGSGSGTDFTLTISLQAEADVAVVYCOQYVSTPYSFGGTLEIK 142

Search completed: March 26, 2004, 05:53:44
Job time : 394.277 sec

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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:17 ; Search time 11.5177 Seconds
(Without alignments)
935.380 Million cell updates/sec

Title: US-10-056-052A-18

Perfect score: 583
Sequence: 1 DIWMTQSPDLSAVSGERVT.....YCHOYLSYTRGGTKLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	530	90.9	111	2	G30502
2	521	89.4	133	1	K4HU1
3	515.5	88.4	114	1	K4HULN
4	514.5	88.3	113	2	S34002
5	514.5	88.3	134	2	S49531
6	513.5	88.1	113	2	S34003
7	512	87.8	112	2	S41393
8	510	87.7	138	2	S26040
9	510	87.5	112	2	S09970
10	507.5	87.0	113	2	S30523
11	507.5	87.0	130	2	S51147
12	507	87.0	103	2	PH1050
13	502.5	86.2	113	2	S30520
14	500	85.8	118	2	PT0356
15	495.5	85.0	114	2	S44116
16	495.5	85.0	240	2	S06084
17	494.5	84.8	114	2	S44119
18	494.5	84.8	145	2	PL0014
19	492.5	84.5	134	1	K4HU17
20	491	84.2	101	2	S26337
21	490.5	84.1	122	2	S46373
22	489	83.9	112	2	S43103
23	489	83.9	113	2	PT0407
24	486	83.4	138	2	A53261
25	485.5	83.3	124	2	S40364
26	484.5	83.1	134	2	PC1214
27	484	83.0	133	2	PS0023
28	483.5	82.9	129	2	S40347
29	480.5	82.4	214	2	S68212

30	479	82.2	121	1	K4HU	Ig kappa chain pre
31	475.5	81.6	113	2	A49260	antitumor monoclon
32	475	81.5	112	2	PL0265	Ig kappa chain V r
33	475	81.5	113	2	PT0408	Ig light chain V r
34	472.5	81.0	113	2	PL0263	Ig kappa chain V r
35	468.5	80.4	113	2	JC2270	PL7-6 antibody 119
36	466.5	80.0	109	2	S26336	Ig light chain V r
37	466	79.9	101	2	PH0869	Ig kappa chain V r
38	465.5	79.8	134	2	S21917	Ig kappa chain V-J
39	464.5	79.7	135	2	S38607	Ig light chain V-J
40	463.5	79.5	220	2	A31790	Ig kappa chain V r
41	463	79.4	106	2	A49138	IgA kappa rheumato
42	462.5	79.3	112	2	E30538	Ig kappa chain V r
43	462.5	79.3	112	2	F30538	Ig kappa chain V r
44	456.5	78.3	113	2	PL0264	Ig kappa chain V r
45	453.5	77.8	136	2	A49137	Ig kappa chain pre

ALIGNMENTS

RESULT 1
G30502
Ig kappa chain V region (A52) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: G30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:86315787; PMID:2457627
A:Accession: G30502
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <EIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F16-96/Domain: immunoglobulin homology <IMV>

Query Match 90.9%; Score 530; DB 2; Length 111;
Best Local Similarity 90.1%; Pred. No. 4.7e-41;
Matches 100; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIWMTQSPDLSAVSGERVTMTNCKSSQSVLYSSNOKYLAHYOQKPCQSPKLTITMASTR 60
DB 1 NIMWTQSPDLSAVSAGEKVTMSCKSSQSVLYSSNOKYLAHYOQKPCQSPKLTITMASTR 60

QY 61 ESGVPRFSGSGGDTFTLTSSVQAEADLAHYCHQYLSYTRGGTKLEI 111
DB 61 ESGVPRFSGSGGDTFTLTSSVQAEADLAHYCHQYLSYTRGGTKLEI 111

RESULT 2
K4HU1
Ig kappa chain precursor V-IV region (J1) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C:Accession: A01904
R:Klobeck, H.G.; Bornkamm, G.W.; Combrat, G.; Mochter, R.; Pontenz, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985
A:Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ!
A:Reference number: A93589; MUID:86041853; PMID:2937712
A:Accession: A01904
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Cross-references: GB:Z00022; GB:X51570; MUD:933158; PIDN:CAA7317.1; PID:9296654
A>Note: The sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV
A:Cross-references: GDB:119341; OMIM:146980
A:Map position: 2p12-2p12
A:introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 14
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Species: Homo sapiens (man)
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-133/Product: Ig kappa chain V-IV region (OI) #status predicted <MAY>
 F:21-43/Region: framework 1
 F:36-116/Domain: immunoglobulin homology <IMM>
 F:44-60/Region: complementarity-determining 1
 F:61-75/Region: complementarity-determining 2
 F:76-82/Region: complementarity-determining 3
 F:83-114/Region: framework 3
 F:115-122/Region: complementarity-determining 3
 F:123-133/Region: framework 4
 F:43-114/Disulfide bonds: #status predicted

Query Match 89.4%; Score 521; DB 1; Length 133;
 Best Local Similarity 89.3%; Pred. No. 3.7e-40;
 Matches 100; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNKNYLAAYQKPGQPKLLIYMASTR 60
 DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAAYQKPGQPKLLIYMASTR 80
 QY 61 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 112
 DB 81 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 132

RESULT 3

KAPHLN
 Ig kappa chain V-IV region (Len) - human

C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
 C:Accession: A01903; F61458
 R:Schneider, M.; Hilschmann, N.
 Hope-Seayler's Z. Physiol. Chem. 356, 507-557, 1975
 A:Title: Die Primerstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV
 A:Reference number: A01903; MUID:76004342; PMID:50295
 A:Accession: A01903
 A:Molecule type: protein
 A:Residues: 1-114 <SCH>
 A:Note: this is the first completely sequenced V region of a new kappa chain subgroup,
 R:Brown, J. C.; Deligi, K.; Gendron, M. C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-assc
 A:Reference number: A61458; MUID:90039128; PMID:2478651
 A:Accession: F61458
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-113 <BRO>
 C:Comment: This is a Bence Jones protein.
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 14
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>
 F:23-94/Disulfide bonds: #status predicted

Query Match 88.4%; Score 515.5; DB 1; Length 114;
 Best Local Similarity 88.5%; Pred. No. 9.8e-40;
 Matches 100; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNKNYLAAYQKPGQPKLLIYMASTR 60
 DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAAYQKPGQPKLLIYMASTR 60
 QY 61 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 112
 DB 61 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 113

RESULT 4

S34002
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S34002; S30522
 R:Marlette, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A:Reference number: S34001; MUID:93209281; PMID:7681398
 A:Accession: S34002
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <MAR>
 A:Cross-references: EMBL:Z18328
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 514.5; DB 2; Length 113;
 Best Local Similarity 88.5%; Pred. No. 1.2e-39;
 Matches 100; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNKNYLAAYQKPGQPKLLIYMASTR 60
 DB 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAAYQKPGQPKLLIYMASTR 60
 QY 61 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 112
 DB 61 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 113

RESULT 5

S49531
 anti-Sm antibody VL chain (V kappa 4/5 kappa 3) - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
 C:Accession: S49531
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A:Reference number: S48797
 A:Accession: S49531
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-124 <MAH>
 A:Cross-references: EMBL:Z46347; NID:G560841; PIDN:CNA6466.1; PID:G560842
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 514.5; DB 2; Length 134;
 Best Local Similarity 87.6%; Pred. No. 1.4e-39;
 Matches 99; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNKNYLAAYQKPGQPKLLIYMASTR 60
 DB 21 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAAYQKPGQPKLLIYMASTR 80
 QY 61 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 112
 DB 81 ESGVPRFSGSGSGTDFTLTITSSVAEDLAVYCHQYLSYTFGGGTKEIK 133

RESULT 6

S34003
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S34003
 R:Marlette, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A:Reference number: S34001; MUID:93209281; PMID:7681398
 A:Accession: S34003

A>Status: preliminary
 A:Molecule type: mRNA
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 88.1%; Score 513.5; DB 2; Length 113;
 Best Local Similarity 88.5%; Pred. No. 1.5e-39;
 Matches 100; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
 DB 1 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60

QY 61 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112
 DB 61 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 113

RESULT 7

S41393
 Ig kappa chain V region (12.5H VL) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
 C:Accession: S41393

R:Margarette, C.; Gilbert, D.; Brard, F.; Tron, F.
 Submitted to the EMBL Data Library, January 1994
 A:Description: Structural characterization of an (NZB X NZW) F1 mouse-derived IGM anti-DK
 A:Reference number: S41393
 A:Accession: S41393

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-112 <MAR>
 C:Cross-references: EMBL:229536
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 512; DB 2; Length 112;
 Best Local Similarity 87.5%; Pred. No. 2e-39;
 Matches 98; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
 DB 1 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60

QY 61 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112
 DB 61 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112

RESULT 8

S26040
 Ig kappa chain precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
 C:Accession: S26040; S78038

R:Okamoto, M.; Honjo, T.
 Nucleic Acids Res 18, 1995, 1990
 A>Title: Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoant
 A:Reference number: S09216; M01D:190245589; PMID:2336568
 C:Accession: S26040

A:Molecule type: DNA
 A:Residues: 1-138 <OKA>
 A:Cross-references: EMBL:X51742
 A>Note: the authors translated the codon AGC for residue 107 as Thr and AGT for residue
 R:Okamoto, M.

Submitted to the EMBL Data Library, February 1990
 A:Reference number: S78098
 A:Accession: S78098
 A:Molecule type: DNA
 A:Residues: 1-87, 'W', 89-138 <OKW>

A:Cross-references: EMBL:X51742; M1D:952697; P1D:CAA36032.1; P1D:952698
 C:Genetics:
 A:Introns: 22/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-25/Domain: signal sequence #status predicted <Sig>
 F:26-138/Product: Ig kappa chain (fragment) #status predicted <Mat>
 F:41-121/Domain: immunoglobulin homology <IMM>

Query Match 87.7%; Score 511; DB 2; Length 138;
 Best Local Similarity 85.7%; Pred. No. 3.1e-39;
 Matches 96; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
 DB 26 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 85

QY 61 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112
 DB 86 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 137

RESULT 9

S09970
 Ig kappa chain V-J region (4C8) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
 C:Accession: S09970

R:Reininger, L.; Shbata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A>Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A:Reference number: S09955; M01D:90269328; PMID:2247362
 A:Accession: S09970

A:Molecule type: mRNA
 A:Residues: 1-112 <REI>
 A:Cross-references: EMBL:X51858; M1D:955406; P1D:CAA36151.1; P1D:930235
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 510; DB 2; Length 112;
 Best Local Similarity 85.7%; Pred. No. 3e-39;
 Matches 96; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60
 DB 1 DIVWTQSPDLSAVSLGERVTNCKSSQSYLYSSNQKNTLAWYQKPGQSPKLLIYMASTR 60

QY 61 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112
 DB 61 ESGVDRFSGSGSGTDFTLTISVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112

RESULT 10

S30523
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S30523

R:Marlette, X.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S30520
 A:Accession: S30523

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <MAR>
 A:Cross-references: EMBL:Z18329
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 507.5; DB 2; Length 113;
 Best Local Similarity 87.6%; Pred. No. 5.1e-39;

A:Reference number: S44105
 A:Accession: S4416
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <HAM>
 A:Cross-references: EMBL:Z11391; NID:G472970; PIDN:CAA83266.1; PID:G940527
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 495.5; DB 2; Length 114;
 Best Local Similarity 85.0%; Pred. No. 6.3e-38;
 Matches 96; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY	1	DIYMTQSPDSIAYISGERVTMNCSSQSVLYSSNCKNYLAWYQKPKQSPKLLIYWA	60
Db	1	DIYMTQSPDSLVVSLGERATINCKSSQSLYSSNNKTYLAWYQKPKQLIKW	60
QY	61	ESGVPPDRFSGSGSGTDFTLTISVCAEDLAVYCHQYLSS-YTFGGGTLEIK	112
Db	61	ESGVPPDRFSGSGSGTDFTLTISLQAEDEVAVFYCQGYTSPLTFGGTVEIK	113

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